GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 15:11:57 ; Search time 3717.85 Seconds
(without alignments)
10265.033 Million cell updates/sec

Title: US-10-070-532-1
Perfect score: 1278
Sequence: 1 atggagccctcagccacccc.....tcaccacagtgctgccctga 1278

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	751.4	58.8	753	29	AY420885	AY420885 Homo sapi
c	2	732.8	57.3	886	13	BX433093	BX433093 BX433093
	3	719.4	56.3	1740	11	BC035686	BC035686 Homo sapi
c	4	692.8	54.2	790	14	CF147830	CF147830 AGENCOURT
c	5	676.4	52.9	899	13	BX433092	BX433092 BX433092
	6	662.8	51.9	750	29	AY420886	AY420886 Pan trogl
	7	578.6	45.3	3470	11	AK048781	AK048781 Mus muscu
	8	578.6	45.3	3729	11	AK038551	AK038551 Mus muscu
	9	575.4	45.0	726	29	AY420887	AY420887 Mus muscu
	10	567.6	44.4	3153	11	AK079572	AK079572 Mus muscu
	11	521	40.8	1790	11	BC035858	BC035858 Homo sapi
	12	470.4	36.8	1001	9	AL535838	AL535838 AL535838
	13	468.4	36.7	520	13	BQ269289	BQ269289 ik23f12.y
	14	437.4	34.2	892	13	BX409735	BX409735 BX409735
	15	393.2	30.8	993	12	BM926746	BM926746 AGENCOURT
c	16	386.8	30.3	625	13	BQ285933	BQ285933 ik23f12.x
	17	376.2	29.4	543	13	BX119589	BX119589 BX119589
	18	367	28.7	788	14	CF147829	CF147829 AGENCOURT
c	19	336.2	26.3	1013	9	AL535837	AL535837 AL535837
	20	330.8	25.9	382	12	BQ042116	BQ042116 sheep1 Sh
c	21	296	23.2	525	12	BI133700	BI133700 UI-M-BH3-
	22	285.4	22.3	635	12	BM939496	BM939496 UI-M-BH3-
	23	265.8	20.8	627	10	BB632359	BB632359 BB632359
	24	265.4	20.8	599	12	BM933820	BM933820 UI-M-BH3-
	25	263.2	20.6	611	13	BY723922	BY723922 BY723922
	26	216.8	17.0	477	12	BM087401	BM087401 500158 MA
	27	206	16.1	552	10	BE863072	BE863072 UI-M-BH0-
	28	202.4	15.8	662	10	BB632883	BB632883 BB632883
	29	199.8	15.6	1073	12	BM920548	BM920548 AGENCOURT
	30	198.4	15.5	245	12	BI976482	BI976482 485407 MA
	31	197.6	15.5	505	10	BB651179	BB651179 BB651179
	32	186.2	14.6	464	13	BY239887	BY239887 BY239887
	33	177	13.8	444	14	R55704	R55704 yg88h10.r1
	34	173.4	13.6	768	13	BX109847	BX109847 BX109847
c	35	167.4	13.1	703	29	CE375359	CE375359 tigr-gss-
	36	163.2	12.8	1290	29	AY411591	AY411591 Homo sapi
	37	162	12.7	721	29	CE235359	CE235359 tigr-gss-
	38	157.8	12.3	1296	29	AY411593	AY411593 Mus muscu
	39	134.6	10.5	257	10	AW427900	AW427900 64510 MAR
c	40	127.2	10.0	1005	28	CC212654	CC212654 CH261-75F
c	41	127.2	10.0	1058	28	CC297061	CC297061 CH261-177
c	42	125.4	9.8	564	13	BU680891	BU680891 UI-CF-EC1
c	43	122.4	9.6	1194	28	CC279941	CC279941 CH261-24C
	44	120.2	9.4	526	29	CG978334	CG978334 CH240_169
	45	120.2	9.4	661	10	BB638470	BB638470 BB638470

ALIGNMENTS

RESULT 1
AY420885
LOCUS AY420885 753 bp DNA linear GSS 17-DEC-2003
DEFINITION Homo sapiens HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY420885
VERSION AY420885.1 GI:39776842
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 753)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 753)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1. .753
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1. .>753
/gene="HCRTR1"
/locus_tag="HCM7373"
ORIGIN

Query Match 58.8%; Score 751.4; DB 29; Length 753;
Best Local Similarity 99.9%; Pred. No. 4.5e-140;
Matches 752; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        526 ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 585
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Db          1 ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 60

Qy        586 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 645
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Db         61 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 120
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Qy        646 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 705
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 180

Qy        706 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 765
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Db        181 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 240

Qy        766 CGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 825
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Db        241 CGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 300

Qy        826 CCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 885
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Db        301 CCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 360

Qy        886 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGC 945
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Db        361 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGC 420

Qy        946 GTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT 1005
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Db        421 GTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT 480

Qy       1006 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC 1065
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Qy       1066 ATCATCTACAACTTCCTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGC 1125
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Db        541 ATCATCTACAACTTCCTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGC 600

Qy       1126 TGCCTGCCTGGCCTGGGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCC 1185
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Db        601 TGCCTGCCTGGCCTGGGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCC 660

Qy       1186 AGCCACAAGTCCTTGTCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTG 1245
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Qy       1246 GTGCTCACCAGCGTCACCACAGTGCTGCCCTGA 1278
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Db        721 GTGCTCACCAGCGTCACCACAGTGCTGCCCTGA 753
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RESULT 2
BX433093/c
LOCUS       BX433093                886 bp    mRNA    linear   EST 15-MAY-2003
DEFINITION  BX433093 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
            CS0DF013YE04 3-PRIME, mRNA sequence.
ACCESSION   BX433093
VERSION     BX433093.1  GI:30779168
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 886)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 151.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAI011ZB01_CS00962_2&cluster=151.r.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAI011ZB01_CS00962_2.

FEATURES Location/Qualifiers
source 1. .886
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF013YE04"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 57.3%; Score 732.8; DB 13; Length 886;
Best Local Similarity 98.9%; Pred. No. 2.6e-136;
Matches 737; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy      377 AGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGT 436
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Db      745 AGGCTGTGTCCGTGTCAGTGACAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGT 686

Qy      437 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCC 496
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Db      685 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATNC 626

Qy      497 TGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCA 556
            |||||||||| |||||||||||||||||||||||||  |||||||||||| ||||||
Db      625 TGGGCATCTGGCCTGTGTCGCTGGCCATCATGGTGCCCAGGGCTGCAGTCATGCAATGCA 566

Qy      557 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT 616
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      565 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT 506

Qy      617 GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGG 676
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Qy        677 CCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCC 736
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Qy        737 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGG 796
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Qy        797 GGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTG 856
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Db        325 GGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTG 266

Qy        857 AAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGG 916
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Db        265 AAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGG 206

Qy        917 TCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGA 976
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Qy        977 TGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGC 1036
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Qy       1037 TGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGCAAATTCC 1096
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Db         85 TGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGCAAATTCC 26

Qy       1097 GGGAGCAGTTTAAGGCTGCCTTCTC 1121
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Db         25 GGGAGCAGTTTAAGGCATCCTTCTC 1
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RESULT 3
BC035686

LOCUS	BC035686 1740 bp mRNA linear HTC 20-SEP-2002
DEFINITION	Homo sapiens, Similar to hypocretin (orexin) receptor 1, clone IMAGE:5750551, mRNA.
ACCESSION	BC035686
VERSION	BC035686.1 GI:23242909
KEYWORDS	HTC.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1740)
AUTHORS	Strausberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 79 Row: m Column: 17
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4557636
This clone has the following problem: frame shifted.

FEATURES Location/Qualifiers
source 1. .1740
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5750551"
/tissue_type="Lung, Spleen, fetal, pooled"
/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 56.3%; Score 719.4; DB 11; Length 1740;
Best Local Similarity 83.5%; Pred. No. 1.7e-133;
Matches 909; Conservative 0; Mismatches 1; Indels 179; Gaps 1;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        506 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 565

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db        566 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGCGATTATCTG 625

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db        626 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 685

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db        686 CTGGTGGGCAACACGCTG---------------------------------------------- 703

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Db        704 ---------------------------------------------------------------- 703
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Qy       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Db       704 ------------------------------------------------------------ 703

Qy       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
                             ||||||||||||||||||||||||||||||||||||||||||
Db       704 -----------------GGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 746

Qy       421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db       747 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 806

Qy       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Qy       541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db       867 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 926

Qy       601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db       927 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 986

Qy       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db       987 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 1046

Qy       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db      1047 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 1106

Qy       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
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Db      1107 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 1166

Qy       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1167 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1226

Qy       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1227 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1286

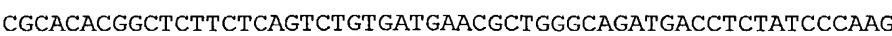
Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1287 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1346

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1347 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1406

Qy      1081 CTCAGTGGC 1089
             |||||||||
Db      1407 CTCAGTGGC 1415
```

RESULT 4
CF147830/c
LOCUS CF147830 790 bp mRNA linear EST 25-JUL-2003
DEFINITION AGENCOURT_14740202 NIH_MGC_145 Homo sapiens cDNA clone IMAGE:6971889 5', mRNA sequence.
ACCESSION CF147830
VERSION CF147830.1 GI:33244098
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 790)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBI02 row: a column: 08
High quality sequence start: 7
High quality sequence stop: 738.
FEATURES Location/Qualifiers
source 1. .790
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971889"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_lib="NIH_MGC_145"
/note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2: varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.data Note: this is a NIH_MGC Library."
ORIGIN

Query Match 54.2%; Score 692.8; DB 14; Length 790;
Best Local Similarity 99.7%; Pred. No. 2.5e-128;
Matches 694; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 583 CGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATC 642


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Db        790 CGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATC 731

Qy        643 TACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCC 702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCC 671

Qy        703 TATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTG 762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 TATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTG 611

Qy        763 GTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGA 822
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Db        610 GTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGA 551

Qy        823 GAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGG 882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGG 491

Qy        883 AAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATC 942
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Db        490 AAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATC 431

Qy        943 AGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAA 1002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 AGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAA 371

Qy       1003 GCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAAC 1062
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Db        370 GCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAAC 311

Qy       1063 CCCATCATCTACAACTTCCTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCC 1122
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Db        310 CCCATCATCTACAACTTCCTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCC 251

Qy       1123 TGCTGCCTGCCTGGCCTGGGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCT 1182
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Db        250 TGCTGCCTGCCTGGCCTGGGCCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCT 191

Qy       1183 GCCAGCCACAAGTCCTTGTCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCAT 1242
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        190 GCCAGCCACAAGTCCTTGTCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCAT 131

Qy       1243 GTGGTGCTCACCAGCGTCACCACAGTGCTGCCCTGA 1278
              ||||||||||||||||||||||||||||||||||||
Db        130 GTGGTGCTCACCAGCGTCACCACAGTGCTGCCCTGA 95
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```
RESULT 5
BX433092/c
LOCUS       BX433092                899 bp    mRNA    linear   EST 15-MAY-2003
DEFINITION  BX433092 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
            CS0DF013YE04 3-PRIME, mRNA sequence.
ACCESSION   BX433092
VERSION     BX433092.1  GI:30779167
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 899)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 151.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAI011ZB01_CS00962_1&cluster=151.r.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAI011ZB01_CS00962_1.

FEATURES Location/Qualifiers
source 1. .899
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF013YE04"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 52.9%; Score 676.4; DB 13; Length 899;
Best Local Similarity 96.6%; Pred. No. 5.2e-125;
Matches 711; Conservative 0; Mismatches 23; Indels 2; Gaps 2;

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Qy        372 TCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCG 431
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Db        738 TGTAAGNNCTGTGTCGTGTTCAGTGGCAGTGCTACTTCTCAGCTTCATCGCCTGGACCCG 679

Qy        432 CTGGTATGCCATC-TGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCT 490
              |||||||||||||  | ||||||||||||||  ||||||||||||||||||||||||||
Db        678 CTGGTATGCCATCATCCCACCCACTATTGTCAAAGAGCACAGCCCGGCGGGCCCGTGCTC 619

Qy        491 CCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGG 550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 CCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGG 559

Qy        551 AATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATG 610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 AATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATG 499

Qy        611 AACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCT 670
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Db        498 AACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCT 439
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Qy        671 ACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGG 730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGG 379

Qy        731 GCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACC 790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 GCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACC 319

Qy        791 AGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCC 850
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Db        318 AGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCC 259

Qy        851 TGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGC 910
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Db        258 TGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGC 199

Qy        911 TGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGT 970
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Db        198 TGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGT 139

Qy        971 TCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCC 1030
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Db        138 TCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCC 79

Qy       1031 ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGCA 1090
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||  |||
Db         78 ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCT-CAACTTCCTCAGGTGCA 20

Qy       1091 AATTCCGGGAGCAGTT 1106
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Db         19 AATTCCGGGAGCAGTT 4
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RESULT 6
AY420886

LOCUS	AY420886	750 bp	DNA	linear	GSS	17-DEC-2003

DEFINITION Pan troglodytes HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY420886
VERSION AY420886.1 GI:39776843
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 750)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 750)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,

```
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence as made by sequencing genomic exons and ordering them
            based on alignment.
FEATURES             Location/Qualifiers
     source          1. .750
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>750
                     /gene="HCRTR1"
                     /locus_tag="HCM7373"
ORIGIN

  Query Match             51.9%;  Score 662.8;  DB 29;  Length 750;
  Best Local Similarity   88.5%;  Pred. No. 2.5e-122;
  Matches  664;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy        526 ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 60

Qy        586 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 645
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Db         61 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 120

Qy        646 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 705
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 180

Qy        706 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 765
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Db        181 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 240

Qy        766 CGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 825
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 300

Qy        826 CCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 885
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Db        301 CCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCGCGGAGGAAG 360

Qy        886 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGC 945
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Db        361 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGT 420

Qy        946 GTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT 1005
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Db        421 GTCCTCAATGTCCTTAAGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 480

Qy       1006 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC 1065
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Db        481 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNACGCCAACAGNNNNGCCAACCCC 540
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Qy       1066 ATCATCTACAACTTCCTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGC 1125
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Db        541 ATCANNNACAACTTCCTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGC 600

Qy       1126 TGCCTGCCTGGCCTGGGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCC 1185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGCCTGCCTGGCCTGGGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCC 660

Qy       1186 AGCCACAAGTCCTTGTCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTG 1245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCCACAAGTCCTTGTCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTG 720

Qy       1246 GTGCTCACCAGCGTCACCACAGTGCTGCCC 1275
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Db        721 GTGCTCACCAGCGTCACCACAGTGCTGCCC 750
```

RESULT 7
AK048781

```
LOCUS       AK048781                3470 bp    mRNA    linear   HTC 20-SEP-2003
DEFINITION  Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length
            enriched library, clone:C230065B06 product:OREXIN RECEPTOR TYPE 2,
            full insert sequence.
ACCESSION   AK048781
VERSION     AK048781.1  GI:26339571
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
```

PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3470)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
FEATURES Location/Qualifiers
source 1. .3470
/organism="Mus musculus"
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/db_xref="FANTOM_DB:C230065B06"
/db_xref="MGI:2415851"
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/clone="C230065B06"
/tissue_type="cerebellum"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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CDS 75. .1457
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Qy         80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
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Qy        500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
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RESULT 8
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LOCUS AK038551 3729 bp mRNA linear HTC 19-SEP-2003
DEFINITION Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230036M08 product:OREXIN RECEPTOR TYPE 2, full insert sequence.
ACCESSION AK038551
VERSION AK038551.1 GI:26332642
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3729)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

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polyA_site 3729
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ORIGIN

Query Match 45.3%; Score 578.6; DB 11; Length 3729;
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Matches 826; Conservative 0; Mismatches 359; Indels 12; Gaps 2;

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Qy         80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
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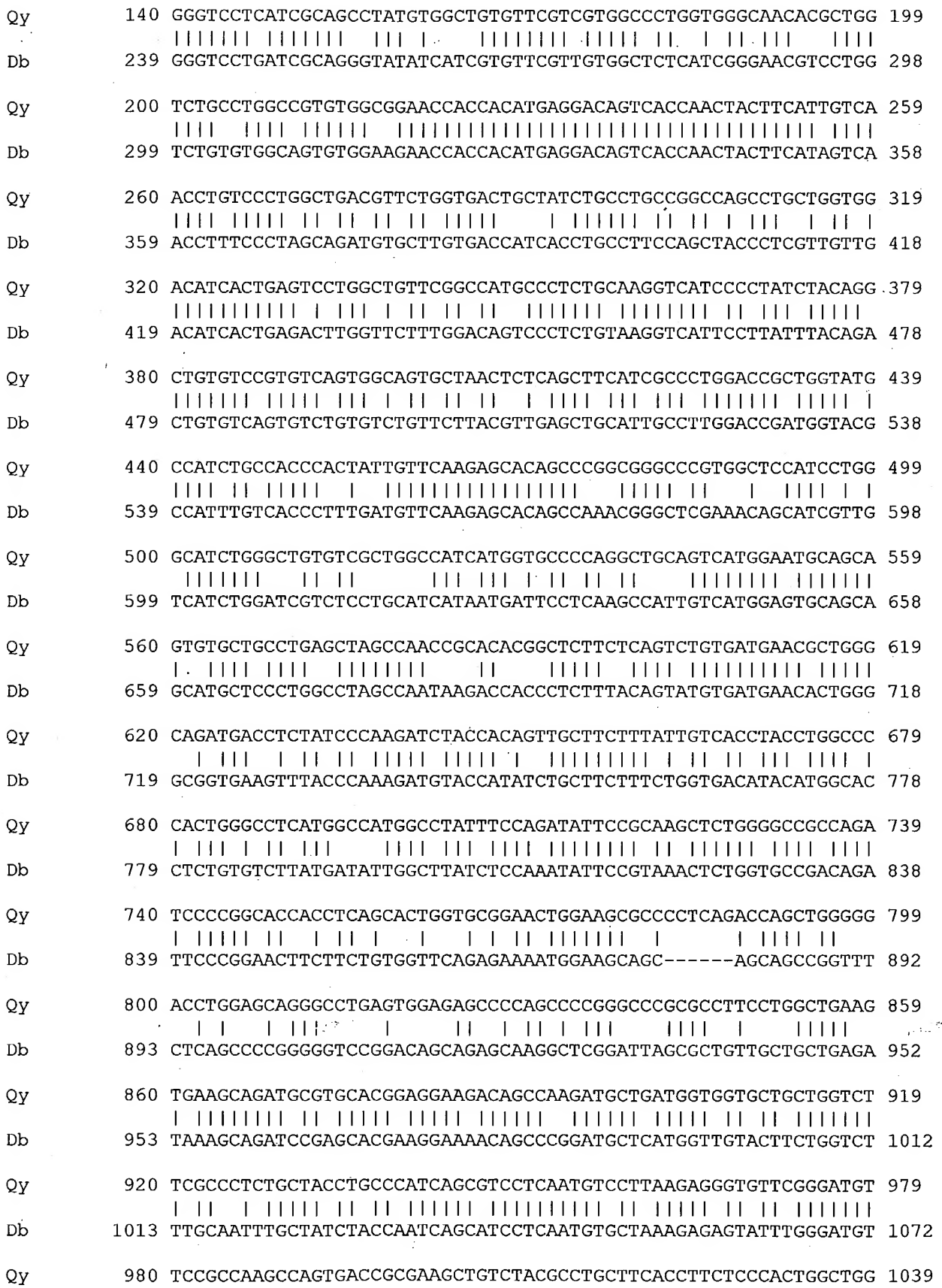

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DEFINITION  Mus musculus HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY420887
VERSION     AY420887.1  GI:39776844
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 726)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 726)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence as made by sequencing genomic exons and ordering them
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ORIGIN

Query Match 45.0%; Score 575.4; DB 29; Length 726;
Best Local Similarity 87.0%; Pred. No. 8e-105;
Matches 655; Conservative 0; Mismatches 71; Indels 27; Gaps 1;

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RESULT 10
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LOCUS       AK079572               3153 bp    mRNA    linear   HTC 19-SEP-2003
DEFINITION  Mus musculus adult male hypothalamus cDNA, RIKEN full-length
            enriched library, clone:A230091E19 product:OREXIN RECEPTOR TYPE 2,
            full insert sequence.
ACCESSION   AK079572
VERSION     AK079572.1  GI:26348079
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
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            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3153)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
```

Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .3153
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:A230091E19"
/db_xref="MGI:2403517"
/db_xref="taxon:10090"
/clone="A230091E19"
/sex="male"
/tissue_type="hypothalamus"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"

CDS 108. .1202
/note="unnamed protein product; OREXIN RECEPTOR TYPE 2 (SWISSPROT|P56719, evidence: FASTY, 98.5%ID, 100%length, match=1380)
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/codon_start=1
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/db_xref="GI:26348080"
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REYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNHHMRTVTNYFIVNLSLADVL
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YPKMYHICFFLVTYMAPLFLMILAYLQIFRKLWCRQIPGTSSVVQRKWKQQQPVSQPR
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ORIGIN

Query Match 44.4%; Score 567.6; DB 11; Length 3153;
Best Local Similarity 68.9%; Pred. No. 5.7e-103;
Matches 826; Conservative 0; Mismatches 359; Indels 13; Gaps 3;

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Qy        80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
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Db       211 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTACACCCGAAAGAATATGAGT 270

Qy       140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
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Db       271 GGGTCCTGATCGCAGGGTATATCATCGTGTTCGTTGTGGCTCTCATCGGGAACGTCCTGG 330

Qy       200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
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Qy       260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
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Db       391 ACCTTTCCCTAGCAGATGTGCTTGTGACCATCACCTGCCTTCCAGCTACCCTCGTTGTTG 450

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Qy        920 TCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979
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Qy       1159 AAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTGTCCTTGCAGAGCCGATGC 1218
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Qy       1219 T------CCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTCACCACAGTGC 1270
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Db       1345 TTTGACAATGTATCAAAACTCTCAGAGCACGTGGTGCTCACCAGCATAAGCACACTCC 1402
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RESULT 11
BC035858
LOCUS       BC035858                1790 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, Similar to hypocretin (orexin) receptor 2, clone
            IMAGE:5767576, mRNA.
ACCESSION   BC035858
VERSION     BC035858.1  GI:23959160
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1790)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
```

Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 79 Row: p Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6006037
This clone has the following problem: retained intron.

FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 40.8%; Score 521; DB 11; Length 1790;
Best Local Similarity 70.3%; Pred. No. 9.5e-94;
Matches 714; Conservative 0; Mismatches 295; Indels 6; Gaps 1;

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Qy         80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
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Qy        260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
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Qy        320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
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Qy        380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
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Qy        440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
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Db        506 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 565

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Db        626 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 685

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Db        686 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 745

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Db        746 CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA 805

Qy        740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG 799

Db        806 TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC------TGCAGCCTGTTT 859

Qy        800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAG 859

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LOCUS       AL535838               1001 bp    mRNA    linear   EST 12-MAY-2003
DEFINITION  AL535838 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
            CS0DF013YE04 5-PRIME, mRNA sequence.
ACCESSION   AL535838
VERSION     AL535838.2  GI:30542758
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1001)
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  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12799331.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 151.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DF013BC02QP1&cluster=151.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DF013BC02QP1.
FEATURES              Location/Qualifiers
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                      /clone="CS0DF013YE04"
                      /tissue_type="FETAL BRAIN"
                      /dev_stage="fetal"
                      /clone_lib="Homo sapiens FETAL BRAIN"
                      /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
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                      vector. Library was not normalized."
ORIGIN

  Query Match             36.8%;  Score 470.4;  DB 9;  Length 1001;
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  Matches  543;  Conservative   13;  Mismatches   26;  Indels    9;  Gaps    6;

Qy        377 AGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGT 436
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Qy        437 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCC 496
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Db        475 ATGCHATCTGCYACCCACTATTGTTCAAGARCACAGCCCGGCGGGCCCGTGGCTCCATCC 534

Qy        497 TGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCA 556
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Db        535 TNNGNATCTGGGCTNTNTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCA 594

Qy        557 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT 616
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Qy        617 GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGG 676
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Qy        796 GGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCT 855
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RESULT 13
BQ269289

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LOCUS       BQ269289                 520 bp    mRNA    linear   EST 15-JUL-2003
DEFINITION  ik23f12.y1 HR85 islet Homo sapiens cDNA clone IMAGE:5782030 5'
            similar to SW:OX1R_HUMAN O43613 OREXIN RECEPTOR TYPE 1 ;, mRNA
            sequence.
ACCESSION   BQ269289
VERSION     BQ269289.1  GI:20494355
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 520)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
            Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
            Williams,T., Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Dr. Hiroshi Inoue
            (hinoue@im.wustl.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 426.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B"
                     /clone_lib="HR85 islet"
                     /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                     NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                     Size-selected on agarose gel. Average insert size ~1kb. 5'
                     XhoI site was destroyed after directional cloning.
                     Amplified once. Contact information: Hiroshi Inoue, MD,
                     Metabolism Div. (Alan Permutt Lab), Washington University
                     School of Medicine, Box 8127, 660 South Euclid Ave., St.
                     Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                     314-362-1916, Fax: 314-747-2692."
ORIGIN

  Query Match             36.7%;  Score 468.4;  DB 13;  Length 520;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-83;
  Matches  469;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        809 AGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGA 868
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGA 60

Qy        869 TGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCT 928
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCT 120

Qy        929 GCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAG 988
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAG 180

Qy        989 CCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCA 1048
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCA 240

Qy       1049 ACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGCAAATTCCGGGAGCAGTTTA 1108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGCAAATTCCGGGAGCAGTTTA 300

Qy       1109 AGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTGGGTCCCTGCGGCTCTCTGAAGGCCCCTA 1168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTGGGTCCCTGCGGCTCTCTGAAGGCCCCTA 360

Qy       1169 GTCCCCGCTCCTCTGCCAGCCACAAGTCCTTGTCCTTGCAGAGCCGATGCTCCGTCTCCA 1228
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        361 GTCCCCGCTCCTCTGCCAGCCACAAGTCCTTGTCCTTGCAGAGCCGATGCTCCATCTCCA 420

Qy       1229 AAATCTCTGAGCATGTGGTGCTCACCAGCGTCACCACAGTGCTGCCCTGA 1278
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAATCTCTGAGCATGTGGTGCTCACCAGCGTCACCACAGTGCTGCCCTGA 470

RESULT 14
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BX409735
LOCUS       BX409735                892 bp    mRNA    linear   EST 13-MAY-2003
DEFINITION  BX409735 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
            CS0DF013YE04 5-PRIME, mRNA sequence.
ACCESSION   BX409735
VERSION     BX409735.1  GI:30652997
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 892)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 151.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0BAF012ZE07_AF01110_1&cluster=151.r.
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0BAF012ZE07_AF01110_1.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="CS0DF013YE04"
                     /tissue_type="FETAL BRAIN"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
ORIGIN

  Query Match             34.2%;  Score 437.4;  DB 13;  Length 892;
  Best Local Similarity   99.8%;  Pred. No. 3.9e-77;
  Matches  438;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        840 CCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCT 899
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCT 60

Qy        900 GATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCT 959
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCT 120

Qy        960 TAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTT 1019
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        121 TAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTT 180

Qy       1020 CACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTT 1079
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTT 240

Qy       1080 CCTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCT 1139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCT 300

Qy       1140 GGGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTT 1199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTT 360

Qy       1200 GTCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGT 1259
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        361 GTCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGT 420

Qy       1260 CACCACAGTGCTGCCCTGA 1278
              ||||||||||||||||||||
Db        421 CACCACAGTGCTGCCCTGA 439
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RESULT 15
BM926746
LOCUS       BM926746                 993 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6681991 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5767576
            5', mRNA sequence.
ACCESSION   BM926746
VERSION     BM926746.1  GI:19377125
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 993)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12826  row: a  column: 17
            High quality sequence stop: 684.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5767576"
                     /lab_host="DH10B"
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/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 30.8%; Score 393.2; DB 12; Length 993;
Best Local Similarity 72.1%; Pred. No. 2.9e-68;
Matches 512; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

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Qy        80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
             | || || || || || || || |||||| | || || ||| |||| ||| | |||||||
Db       145 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 204

Qy       140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
             ||||||| ||||| |  ||  |    |||||||||||||| ||  | || |||   ||||
Db       205 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 264

Qy       200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
             | ||  |||| ||||||  |||||||||||||||||| || ||||||||||||| ||||
Db       265 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 324

Qy       260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
             | || || |||||||| || || |||||    | |||||| || ||||  ||| | ||||
Db       325 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 384

Qy       320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
             | ||||||||| ||||| | || || ||  |||| ||||| || || || |||||||||
Db       385 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 444

Qy       380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
             | ||||| ||||| ||| | || || || || |||| |||||| |||| || |||||||
Db       445 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 504

Qy       440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
             | ||||| |||||  |  |||| ||||||||||   |||||||||  |  |||  |
Db       505 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 564

Qy       500 GCATCTGGCCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
              |||||||  ||| ||       || ||| | || |||||    |||||||| |||||||
Db       565 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 624

Qy       560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
              ||| | || |   |||||||    ||    |||||  | || |||||||| |||||||
Db       625 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 684

Qy       620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
              | |||  | |||||||||| |||||||  || |||||| | || || ||| |||| |
Db       685 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 744
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Qy        680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
              ||||| | |||||||  ||||| ||| | || ||||| ||||| |||||| | || ||||
Db        745 CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA 804

Qy        740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGAC 789
              |||| || ||  | || | | |   | | || |||||   |||   || |
Db        805 TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAAGCCCCTGGAGCC 854
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Search completed: October 15, 2004, 22:50:27
Job time : 3725.85 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 13:54:41 ; Search time 5178.06 Seconds
(without alignments)
10697.520 Million cell updates/sec

Title: US-10-070-532-1
Perfect score: 1278
Sequence: 1 atggagccctcagccacccc.....tcaccacagtgctgccctga 1278

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
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24: em_ph:*
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28: em_un:*
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31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1274.8	99.7	1564	6	E43974	E43974 Novel G pro
2	1274.8	99.7	1564	6	E50810	E50810 Novel G pro
3	1274.8	99.7	1564	6	E50811	E50811 Novel G pro
4	1274.8	99.7	1564	6	AX299473	AX299473 Sequence
5	1274.8	99.7	1564	6	AX299475	AX299475 Sequence
6	1274.8	99.7	1564	6	AX549082	AX549082 Sequence
7	1274.8	99.7	1564	6	AX746121	AX746121 Sequence
8	1274.8	99.7	1564	6	AX840912	AX840912 Sequence
9	1274.8	99.7	1564	9	AF041243	AF041243 Homo sapi
10	1270	99.4	1278	6	AX280925	AX280925 Sequence
11	1205.8	94.4	1209	6	AR216117	AR216117 Sequence
12	1201	94.0	1209	6	BD185452	BD185452 Human neu
13	1086.4	85.0	1133	6	E43973	E43973 Novel G pro
14	1086.4	85.0	1133	6	AX746120	AX746120 Sequence
15	1086.4	85.0	1170	6	E43972	E43972 Novel G pro
16	1086.4	85.0	1170	6	AX746118	AX746118 Sequence
17	1085.8	85.0	1110	6	AR216118	AR216118 Sequence
18	1083.2	84.8	1116	6	AR216119	AR216119 Sequence
19	1083.2	84.8	1133	6	BD185454	BD185454 Human neu
20	1077.8	84.3	1110	6	BD185453	BD185453 Human neu
21	998	78.1	2200	10	AY336083	AY336083 Mus muscu
22	991.6	77.6	2469	10	AF041244	AF041244 Rattus no
23	699.2	54.7	843	6	AR109899	AR109899 Sequence
24	672.2	52.6	789	6	AR109632	AR109632 Sequence
25	672.2	52.6	789	6	E12154	E12154 cDNA encodi
26	672.2	52.6	789	6	AR300942	AR300942 Sequence
27	640.2	50.1	781	10	AF394596	AF394596 Mus muscu
28	601.2	47.0	3114	10	AF041246	AF041246 Rattus no
29	578.6	45.3	1545	10	AY336084	AY336084 Mus muscu
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31	554.4	43.4	1633	6	E33974	E33974 cDNA clone
32	554.4	43.4	1843	6	AX549084	AX549084 Sequence
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34	554.4	43.4	1878	9	AF041245	AF041245 Homo sapi
35	549.6	43.0	1335	6	AX280927	AX280927 Sequence
36	541.6	42.4	1805	4	AF164626	AF164626 Canis fam
37	497.8	39.0	597	10	AY255599	AY255599 Mus muscu
38	330.8	25.9	382	4	AF499612	AF499612 Ovis arie
39	304.2	23.8	637	10	AF394597	AF394597 Mus muscu
40	281.6	22.0	328	4	AB092488	AB092488 Bos tauru
41	263.2	20.6	501	4	AF532967	AF532967 Ovis arie
42	249.2	19.5	344	9	F202078S03	AF202080 Homo sapi
43	249.2	19.5	9785	6	AR178605	AR178605 Sequence
44	249.2	19.5	9785	6	AX088174	AX088174 Sequence
45	249.2	19.5	9785	9	AY062030	AY062030 Homo sapi

ALIGNMENTS

RESULT 1
E43974
LOCUS E43974 1564 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel G protein-coupled receptor (HFGAN72Y).
ACCESSION E43974
VERSION E43974.1 GI:18625173
KEYWORDS JP 2000106888-A/3.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 1564)
AUTHORS Bergsma,D.J. and Ellis,C.E.
TITLE Novel G protein-coupled receptor (HFGAN72Y)
JOURNAL Patent: JP 2000106888-A 3 18-APR-2000;
SMITHKLINE BEECHAM CORP
COMMENT OS Unidentified
PN JP 2000106888-A/3
PD 18-APR-2000
PF 21-JUL-1999 JP 1999206116
PR 30-APR-1997 US 08/846705
PI DERK J BERGSMA,CATHARINE ELIZABETH ELLIS
PC C12N15/09,A61K38/00,A61K38/00,A61K45/00,A61K48/00,A61P1/00, PC
A61P1/14,
PC A61P9/02,A61P9/04,A61P9/10,A61P9/12,A61P11/06,A61P13/02, PC
A61P13/08,
PC A61P19/10,A61P25/14,A61P25/16,A61P25/18,A61P25/22,A61P25/24,
PC A61P31/04,
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PC A61P43/00,
PC C07K14/705,C07K16/28,C12N1/21,C12N5/10,C12P21/02,G01N33/566,
PC G01N33/577//
PC C12P21/08,(C12N15/09,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,
PC A61K37/02,
PC A61K37/02,C12N5/00,(C12N15/00,C12R1:91)
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1. .1564
FT /organism='Unidentified'.
FEATURES Location/Qualifiers

source 1. .1564
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/db_xref="taxon:32644"

ORIGIN

Query Match 99.7%; Score 1274.8; DB 6; Length 1564;
Best Local Similarity 99.8%; Pred. No. 9.4e-244;
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873
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Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
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Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
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Db       1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
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Db       1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
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Db       1354 TCCTTGTAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy       1261 ACCACAGTGCTGCCCTGA 1278
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Db       1414 ACCACAGTGCTGCCCTGA 1431
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RESULT 2
E50810
LOCUS       E50810                  1564 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Novel G protein-bound receptor (HFGAN 72X).
ACCESSION   E50810
VERSION     E50810.1  GI:13023197
KEYWORDS    JP 2000060578-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1564)
  AUTHORS   Derk,J.B. and Catharine,E.E.
  TITLE     Novel G protein-bound receptor (HFGAN 72X)
  JOURNAL   Patent: JP 2000060578-A 1 29-FEB-2000;
            SMITHKLINE BEECHAM CORP
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COMMENT      OS   Unidentified
             PN   JP 2000060578-A/1
             PD   29-FEB-2000
             PF   21-JUL-1999 JP 1999206115
             PR   30-APR-1997 US    08/846704
             PI   DERK J BERGSMA,CATHARINE ELIZABETH ELLIS
             PC   C12N15/09,A61K31/70,A61K38/00,A61K39/00,A61K39/395,A61K39/395,
             PC   A61K45/00,
             PC   A61K48/00,A61P3/04,A61P9/00,A61P11/06,A61P13/00,A61P25/00, PC
              A61P25/16,
             PC   A61P25/18,A61P25/20,A61P25/22,A61P31/04,A61P31/10,A61P31/12,
             PC   A61P31/18,
             PC   A61P35/00,A61P37/00,C07K14/705,C12N5/10,C12P21/02,C12Q1/02, PC
               G01N33/53,
             PC   G01N33/566//C07K16/28,C12N15/00,A61K37/02,C12N5/00 CC
             Strandedness: Single;
             CC   Topology: Linear;
             FH   Key             Location/Qualifiers
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             FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             99.7%;  Score 1274.8;  DB 6;  Length 1564;
  Best Local Similarity   99.8%;  Pred. No. 9.4e-244;
  Matches 1276;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
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Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
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Db       1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
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Db       1354 TCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413
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Qy       1261 ACCACAGTGCTGCCCTGA 1278
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Db       1414 ACCACAGTGCTGCCCTGA 1431


RESULT 3
E50811
LOCUS       E50811                  1564 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Novel G protein-bound receptor (HFGAN 72X).
ACCESSION   E50811
VERSION     E50811.1  GI:13023198
KEYWORDS    JP 2000060578-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1564)
  AUTHORS   Derk,J.B. and Catharine,E.E.
  TITLE     Novel G protein-bound receptor (HFGAN 72X)
  JOURNAL   Patent: JP 2000060578-A 2 29-FEB-2000;
            SMITHKLINE BEECHAM CORP
COMMENT     OS   Unidentified
            PN   JP 2000060578-A/2
            PD   29-FEB-2000
            PF   21-JUL-1999 JP 1999206115
            PR   30-APR-1997 US    08/846704
            PI   DERK J BERGSMA,CATHARINE ELIZABETH ELLIS
            PC   C12N15/09,A61K31/70,A61K38/00,A61K39/00,A61K39/395,A61K39/395,
            PC   A61K45/00,
            PC   A61K48/00,A61P3/04,A61P9/00,A61P11/06,A61P13/00,A61P25/00, PC
             A61P25/16,
            PC   A61P25/18,A61P25/20,A61P25/22,A61P31/04,A61P31/10,A61P31/12,
            PC   A61P31/18,
            PC   A61P35/00,A61P37/00,C07K14/705,C12N5/10,C12P21/02,C12Q1/02, PC
              G01N33/53,
            PC   G01N33/566//C07K16/28,C12N15/00,A61K37/02,C12N5/00 CC
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            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
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            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             99.7%;  Score 1274.8;  DB 6;  Length 1564;
  Best Local Similarity   99.8%;  Pred. No. 9.4e-244;
  Matches 1276;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
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Db       1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
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Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
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Db       1354 TCCTTGTAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy       1261 ACCACAGTGCTGCCCTGA 1278
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Db       1414 ACCACAGTGCTGCCCTGA 1431
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RESULT 4
AX299473
LOCUS       AX299473                1564 bp    DNA     linear   PAT 26-NOV-2001
DEFINITION  Sequence 1 from Patent EP1154019.
ACCESSION   AX299473
VERSION     AX299473.1  GI:17129230
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE     G-protein coupled receptor (hfgan72x)
  JOURNAL   Patent: EP 1154019-A 1 14-NOV-2001;
            SmithKline Beecham Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .1564
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ORIGIN

  Query Match             99.7%;  Score 1274.8;  DB 6;  Length 1564;
  Best Local Similarity   99.8%;  Pred. No. 9.4e-244;
  Matches 1276;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213
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Qy        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db       214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy       121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db       274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

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Qy       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db       394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

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Db       454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Qy       421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Qy       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db       634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy       541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db       694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy       601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db       754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db       874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db       994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053
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Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
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Db       1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
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Db       1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
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Db       1354 TCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy       1261 ACCACAGTGCTGCCCTGA 1278
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Db       1414 ACCACAGTGCTGCCCTGA 1431
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RESULT 5
AX299475
LOCUS       AX299475                1564 bp    DNA     linear   PAT 26-NOV-2001
DEFINITION  Sequence 3 from Patent EP1154019.
ACCESSION   AX299475
VERSION     AX299475.1  GI:17129231
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE     G-protein coupled receptor (hfgan72x)
  JOURNAL   Patent: EP 1154019-A 3 14-NOV-2001;
            SmithKline Beecham Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .1564
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ORIGIN

  Query Match             99.7%;  Score 1274.8;  DB 6;  Length 1564;
  Best Local Similarity   99.8%;  Pred. No. 9.4e-244;
  Matches 1276;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
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Db       1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
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Db       1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
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Db       1354 TCCTTGTAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy       1261 ACCACAGTGCTGCCCTGA 1278
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Db       1414 ACCACAGTGCTGCCCTGA 1431
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RESULT 6
AX549082
LOCUS       AX549082               1564 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 367 from Patent WO02061087.
ACCESSION   AX549082
VERSION     AX549082.1  GI:25813851
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Burmer,G.C., Roush,C.L. and Brown,J.P.
  TITLE     Antigenic peptides, such as for G protein-coupled receptors
            (GPCRs), antibodies thereto, and systems for identifying such
            antigenic peptides
  JOURNAL   Patent: WO 02061087-A 367 08-AUG-2002;
            Lifespan Biosciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1564
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match             99.7%;  Score 1274.8;  DB 6;  Length 1564;
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Best Local Similarity 99.8%; Pred. No. 9.4e-244;
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

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Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
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Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
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Db       1354 TCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy       1261 ACCACAGTGCTGCCCTGA 1278
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Db       1414 ACCACAGTGCTGCCCTGA 1431


RESULT 7
AX746121
LOCUS       AX746121               1564 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4 from Patent EP1156110.
ACCESSION   AX746121
VERSION     AX746121.1  GI:31744927
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE     G-protein coupled receptor (HFGAN72Y)
  JOURNAL   Patent: EP 1156110-A 4 21-NOV-2001;
            SMITHKLINE BEECHAM CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .1564
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /note="HGS EST 554692"
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ORIGIN

Query Match 99.7%; Score 1274.8; DB 6; Length 1564;
Best Local Similarity 99.8%; Pred. No. 9.4e-244;
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

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Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
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Qy       1261 ACCACAGTGCTGCCCTGA 1278
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Db       1414 ACCACAGTGCTGCCCTGA 1431
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RESULT 8
AX840912
LOCUS       AX840912               1564 bp    DNA     linear   PAT 16-DEC-2003
DEFINITION  Sequence 8 from Patent WO03075945.
ACCESSION   AX840912
VERSION     AX840912.1  GI:39979051
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Eulenberg,K., Steuernagel,A., Haeder,T. and Broenner,G.
  TITLE     Cg8327, cg10823, cg18418, cg15862, cg3768, cg11447 and cg16750
            homologous proteins involved in the regulation of energy
            homeostasis
  JOURNAL   Patent: WO 03075945-A 8 18-SEP-2003;
            DeveloGen Aktiengesellschaft fuer entwicklungsbiologische;
            Forschung (DE)
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FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             99.7%;  Score 1274.8;  DB 6;  Length 1564;
  Best Local Similarity   99.8%;  Pred. No. 9.4e-244;
  Matches 1276;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

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Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
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DEFINITION  Homo sapiens orexin receptor-1 mRNA, complete cds.
ACCESSION   AF041243
VERSION     AF041243.1  GI:2897123
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 1564)
  AUTHORS   Sakurai,T., Amemiya,A., Ishii,M., Matsuzaki,I., Chemelli,R.M.,
            Tanaka,H., Williams,S.C., Richardson,J.A., Kozlowski,G.P.,
```

Wilson,S., Arch,J.R.S., Buckingham,R.E., Haynes,A.C., A. Carr,S.A., Annan,R.S., McNulty,D.E., Liu,W.-S., Terrett,J.A., Elshourbagy,N.A., Bergsma,D.J. and Yanagisawa,M.

TITLE Orexins and orexin receptors: a family of hypothalamic neuropeptides and G protein-coupled receptors that regulate feeding behavior

JOURNAL Cell 92 (4), 573-585 (1998)

MEDLINE 98150861

PUBMED 9491897

REFERENCE 2 (bases 1 to 1564)

AUTHORS Sakurai,T., Amemiya,A., Ishii,M., Matsuzaki,I., Chemelli,R.M., Tanaka,H., Williams,S.C., Richardson,J.A., Kozlowski,G.P., Wilson,S., Arch,J.R.S., Buckingham,R.E., Haynes,A.C., A. Carr,S.A., Annan,R.S., McNulty,D.E., Liu,W.-S., Terrett,J.A., Elshourbagy,N.A., Bergsma,D.J. and Yanagisawa,M.

TITLE Direct Submission

JOURNAL Submitted (07-JAN-1998) HHMI/Department of Molecular Genetics, University of Texas Southwestern Medical Center at Dallas, 5323 Harry Hines Blvd., Rm. Y5.224, Dallas, TX 75235-9050, USA

FEATURES Location/Qualifiers

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ORIGIN

Query Match 99.7%; Score 1274.8; DB 9; Length 1564;
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Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db       1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

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Db       1414 ACCACAGTGCTGCCCTGA 1431
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RESULT 10
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DEFINITION  Sequence 548 from Patent WO0177172.
ACCESSION   AX280925
VERSION     AX280925.1  GI:16608218
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lehmann-Bruinsma,K., Liaw,C.W. and Lin,I.L.
  TITLE     Non-endogenous, consstitutively activated known g protein-coupled
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  JOURNAL   Patent: WO 0177172-A 548 18-OCT-2001;
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ORIGIN

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Db       1261 ACCACAGTGCTGCCCTGA 1278
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RESULT 11
AR216117

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DEFINITION  Sequence 1 from patent US 6410701.
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VERSION     AR216117.1  GI:23314430
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1209)
  AUTHORS   Soppet,D.R., Li,Y. and Rosen,C.A.
  TITLE     Human neuropeptide receptor
  JOURNAL   Patent: US 6410701-A 1 25-JUN-2002;
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match 94.4%; Score 1205.8; DB 6; Length 1209;
Best Local Similarity 99.8%; Pred. No. 5.4e-230;
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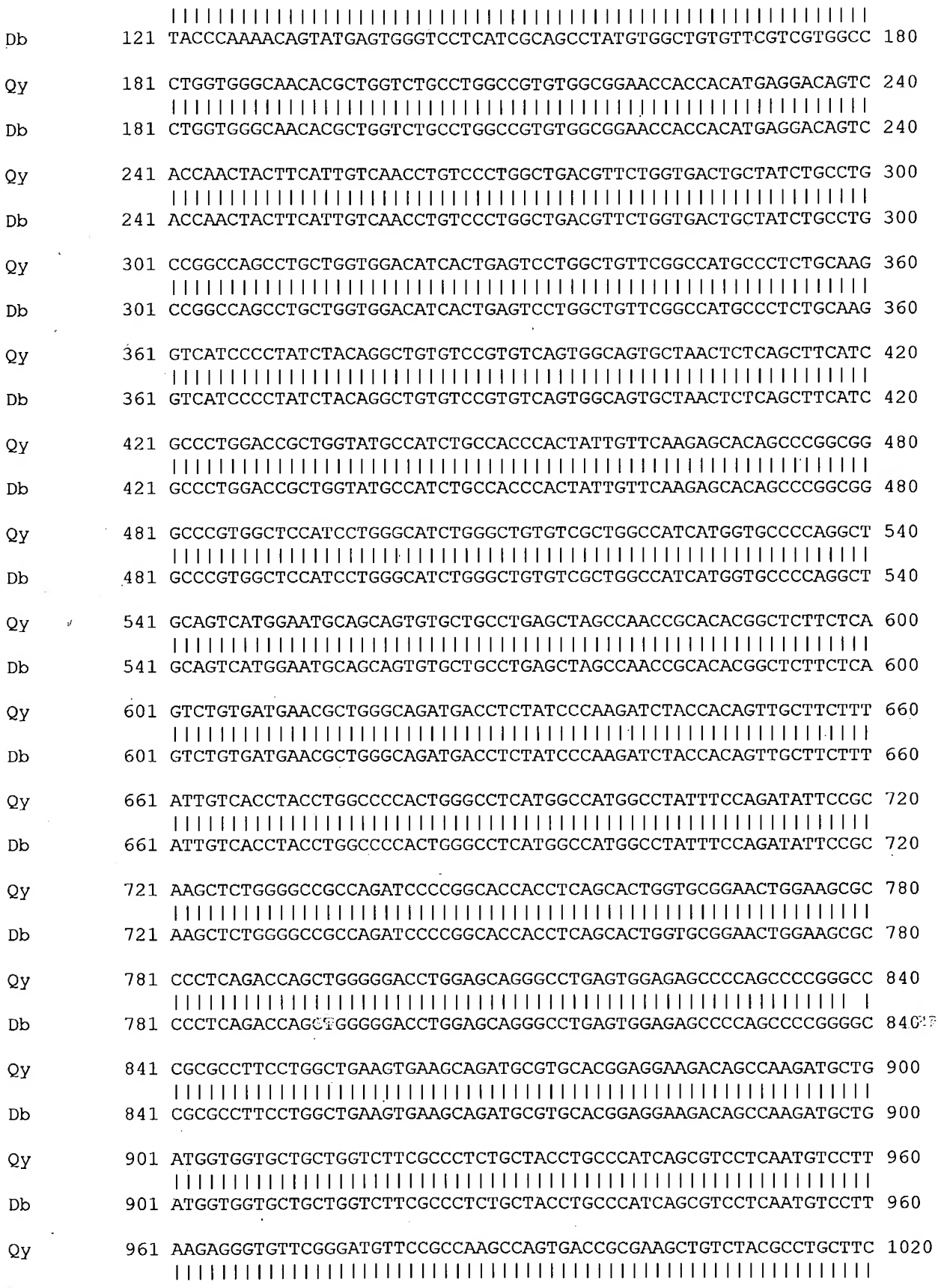

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Qy       1201 TCCTTGCAG 1209
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Db       1201 TCCTTGTAG 1209


RESULT 12
BD185452
LOCUS       BD185452                1209 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  Human neuropeptide receptor.
ACCESSION   BD185452
VERSION     BD185452.1  GI:31877652
KEYWORDS    JP 2002360288-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1209)
  AUTHORS   Soppet,D.R., Li,Y. and Rosen,C.A.
  TITLE     Human neuropeptide receptor
  JOURNAL   Patent: JP 2002360288-A 1 17-DEC-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Unidentified
            PN   JP 2002360288-A/1
            PD   17-DEC-2002
            PF   02-MAY-2002 JP 2002130838
            PI   DANIEL R SOPPET,YI LI,CRAIG A ROSEN
            PC   C12N15/09,A61K31/7088,A61K38/00,A61K45/00,A61K48/00,A61P3/04,
            PC   A61P3/06,
            PC   A61P3/10,A61P9/10,A61P9/12,A61P25/08,A61P25/18,A61P25/22, PC
           A61P25/28,
            PC   A61P35/00,A61P43/00,C07K14/705,C07K16/24,C12N1/15,C12N1/19, PC
              C12N1/21,
            PC   C12N5/10,C12Q1/68,C12N15/00,C12N5/00,A61K37/02 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   Human neuropeptide receptor
            FH   Key             Location/Qualifiers
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            FT                   /organism='Unidentified'.
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ORIGIN

Query Match 94.0%; Score 1201; DB 6; Length 1209;
Best Local Similarity 99.6%; Pred. No. 4.8e-229;
Matches 1204; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCCCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
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Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

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Db       1201 TCCTTGTAG 1209
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RESULT 13
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LOCUS       E43973                 1133 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Novel G protein-coupled receptor (HFGAN72Y).
ACCESSION   E43973
VERSION     E43973.1  GI:18625172
KEYWORDS    JP 2000106888-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1133)
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE     Novel G protein-coupled receptor (HFGAN72Y)
  JOURNAL   Patent: JP 2000106888-A 2 18-APR-2000;
            SMITHKLINE BEECHAM CORP
COMMENT     OS   Unidentified
            PN   JP 2000106888-A/2
            PD   18-APR-2000
            PF   21-JUL-1999 JP 1999206116
            PR   30-APR-1997 US    08/846705
            PI   DERK J BERGSMA,CATHARINE ELIZABETH ELLIS
            PC   C12N15/09,A61K38/00,A61K38/00,A61K45/00,A61K48/00,A61P1/00, PC
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PC A61P9/02,A61P9/04,A61P9/10,A61P9/12,A61P11/06,A61P13/02, PC A61P13/08,
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PC G01N33/577//
PC C12P21/08,(C12N15/09,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,
PC A61K37/02,
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CC Topology: Linear;
FH Key Location/Qualifiers
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ORIGIN

Query Match 85.0%; Score 1086.4; DB 6; Length 1133;
Best Local Similarity 99.9%; Pred. No. 3.3e-206;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db       1081 CTCAGTGG 1088
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RESULT 14
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DEFINITION  Sequence 3 from Patent EP1156110.
ACCESSION   AX746120
VERSION     AX746120.1  GI:31744926
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Bergsma,D.J. and Ellis,C.E.
TITLE G-protein coupled receptor (HFGAN72Y)
JOURNAL Patent: EP 1156110-A 3 21-NOV-2001;
SMITHKLINE BEECHAM CORPORATION (US)

FEATURES Location/Qualifiers
source 1. .1133
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ORIGIN

Query Match 85.0%; Score 1086.4; DB 6; Length 1133;
Best Local Similarity 99.9%; Pred. No. 3.3e-206;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
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Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Qy       1081 CTCAGTGG 1088
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RESULT 15
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LOCUS       E43972                  1170 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Novel G protein-coupled receptor (HFGAN72Y).
ACCESSION   E43972
VERSION     E43972.1  GI:18625171
KEYWORDS    JP 2000106888-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1170)
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE     Novel G protein-coupled receptor (HFGAN72Y)
  JOURNAL   Patent: JP 2000106888-A 1 18-APR-2000;
            SMITHKLINE BEECHAM CORP
COMMENT     OS   Unidentified
            PN   JP 2000106888-A/1
            PD   18-APR-2000
            PF   21-JUL-1999 JP 1999206116
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PC C12N15/09,A61K38/00,A61K38/00,A61K45/00,A61K48/00,A61P1/00, PC
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PC C07K14/705,C07K16/28,C12N1/21,C12N5/10,C12P21/02,G01N33/566,
PC G01N33/577//
PC C12P21/08,(C12N15/09,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,
PC A61K37/02,
PC A61K37/02,C12N5/00,(C12N15/00,C12R1:91)
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1. .1170
FT /organism='Unidentified'.

FEATURES Location/Qualifiers
source 1. .1170
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/mol_type="genomic DNA"
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ORIGIN

Query Match 85.0%; Score 1086.4; DB 6; Length 1170;
Best Local Similarity 99.9%; Pred. No. 3.3e-206;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
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Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
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Db       1081 CTCAGTGG 1088


Search completed: October 15, 2004, 19:59:34
Job time : 5183.06 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 13:52:46 ; Search time 545.899 Seconds
(without alignments)
9945.416 Million cell updates/sec

Title: US-10-070-532-1
Perfect score: 1278
Sequence: 1 atggagccctcagccacccc.....tcaccacagtgctgccctga 1278

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1278	100.0	1278	4	AAS00491	Aas00491 Human neu
2	1274.8	99.7	1564	2	AAV63468	Aav63468 cDNA enco
3	1274.8	99.7	1564	2	AAV68514	Aav68514 Nucleotid
4	1274.8	99.7	1564	4	AAS17464	Aas17464 Human G p
5	1274.8	99.7	1564	4	AAF32103	Aaf32103 Human HFG
6	1274.8	99.7	1564	6	ABA96021	Aba96021 HGS EST 5
7	1274.8	99.7	1564	6	AAI64173	Aai64173 HFGAN72X

8	1274.8	99.7	1564	6	AAI64172	Aai64172 Human HFG
9	1274.8	99.7	1564	7	ABZ42789	Abz42789 Human ore
10	1270	99.4	1278	5	ABI98014	Abi98014 Non-endog
11	1225.2	95.9	1278	4	AAD09335	Aad09335 Cynomolgo
12	1202.6	94.1	1209	2	AAT42826	Aat42826 Neuropept
13	1086.4	85.0	1133	2	AAV68512	Aav68512 Nucleotid
14	1086.4	85.0	1133	6	ABA96020	Aba96020 HGS EST 5
15	1086.4	85.0	1170	2	AAV68511	Aav68511 Nucleotid
16	1086.4	85.0	1170	6	ABA96019	Aba96019 G-protein
17	1085.8	85.0	1110	2	AAT42827	Aat42827 Neuropept
18	1084.8	84.9	1133	4	AAS00493	Aas00493 Human neu
19	1083.2	84.8	1133	2	AAT42828	Aat42828 Neuropept
20	1083	84.7	1281	5	AAC85974	Aac85974 Dog orexi
21	1077.8	84.3	1110	4	AAS00492	Aas00492 Human neu
22	672.2	52.6	789	2	AAT13909	Aat13909 Rabbit G-
23	672.2	52.6	789	2	AAT51065	Aat51065 G-protein
24	554.4	43.4	1633	2	AAX29700	Aax29700 Human 7-t
25	554.4	43.4	1843	7	ABZ42790	Abz42790 Human ore
26	549.6	43.0	1335	4	AAF90300	Aaf90300 Nucleotid
27	549.6	43.0	1335	5	ABI98015	Abi98015 Non-endog
28	249.2	19.5	344	5	AAF56748	Aaf56748 Human HCR
29	249.2	19.5	9785	5	AAF55159	Aaf55159 Nucleotid
30	249.2	19.5	10453	4	AAS17462	Aas17462 Human G p
31	244	19.1	244	4	AAS17449	Aas17449 Human G p
32	231.6	18.1	331	5	AAF56750	Aaf56750 Human HCR
33	227	17.8	227	4	AAS17453	Aas17453 Human G p
34	199	15.6	356	4	AAS17445	Aas17445 Human G p
35	198.6	15.5	452	5	AAF56746	Aaf56746 Human HCR
36	191.6	15.0	374	5	AAF56752	Aaf56752 Human HCR
37	189.4	14.8	324	4	AAS17457	Aas17457 Human G p
38	188.8	14.8	1287	2	AAV68513	Aav68513 Nucleotid
39	188.8	14.8	1287	6	ABA96022	Aba96022 Sac I sub
40	181	14.2	263	5	AAF56747	Aaf56747 Human HCR
41	179	14.0	179	4	AAS17447	Aas17447 Human G p
42	163.2	12.8	1290	3	AAA70507	Aaa70507 Novel hum
43	163.2	12.8	1290	3	AAA70508	Aaa70508 Novel hum
44	163.2	12.8	1290	4	AAH78518	Aah78518 Nucleotid
45	163.2	12.8	1290	4	AAH78519	Aah78519 Nucleotid

ALIGNMENTS

RESULT 1
AAS00491
ID AAS00491 standard; cDNA; 1278 BP.
XX
AC AAS00491;
XX
DT 17-MAY-2001 (first entry)
XX
DE Human neuropeptide receptor cDNA.
XX
KW Human; neuropeptide receptor; neuropeptide Y receptor; obesity;
KW nervous system disorder; hyperproliferative disorder; diabetes mellitus;
KW cardiovascular disorder; autoimmune disorder; infectious disorder;
KW eating behaviour disorder; narcolepsy; neurological disease;

KW narcotics addiction; nicotine addiction; alcohol addiction; gene therapy;
KW protein co-ordinate data; chromosome 1; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1278
FT /*tag= a
FT /product= "neuropeptide receptor"
XX
PN WO200117532-A1.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024518.
XX
PR 10-SEP-1999; 99US-00393696.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Soppet DR, Li Y, Rosen CA;
XX
DR WPI; 2001-183276/18.
DR P-PSDB; AAU00438.
XX
PT A new nucleic acid encoding a human neuropeptide receptor polypeptide,
PT useful for preventing, treating or ameliorating obesity, narcolepsy,
PT neurological disease and addiction to narcotics, nicotine and alcohol.
XX
PS Claim 4; Fig 1; 385pp; English.
XX
CC The present sequence encodes for a novel human neuropeptide receptor
CC which shows sequence homology to the neuropeptide Y receptor. Two splice
CC variants of the neuropeptide receptor (AAU00439-AAU00440) and a possible
CC mutant (AAU00442) are also described. Polypeptides and polynucleotides of
CC the neuropeptide receptor are useful for diagnosing, preventing, or
CC treating a pathological condition in a subject related to the central
CC nervous and peripheral nervous systems (CNS and PNS). The polypeptides
CC and polynucleotides may be used to treat hyperproliferative,
CC cardiovascular, autoimmune, nervous system or infectious disorders e.g.
CC cancer, heart disease, rheumatoid arthritis, Alzheimer's disease, HIV
CC infection and diabetes mellitus. In particular they are useful for
CC preventing, treating or ameliorating a medical condition in a mammal such
CC as obesity/eating behaviour disorders, narcolepsy, neurological disease,
CC addiction to narcotics, nicotine and alcohol, chronic pain, acute pain,
CC migraine headaches and anxiety disorders. The polynucleotides encoding
CC the neuropeptide receptor can also be used in gene therapy methods for
CC treating such diseases
XX
SQ Sequence 1278 BP; 220 A; 426 C; 347 G; 285 T; 0 U; 0 Other;

Query Match 100.0%; Score 1278; DB 4; Length 1278;
Best Local Similarity 100.0%; Pred. No. 3.1e-289;
Matches 1278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

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Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
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Db       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200

Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
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Qy       1261 ACCACAGTGCTGCCCTGA 1278
              ||||||||||||||||||
Db       1261 ACCACAGTGCTGCCCTGA 1278
```

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RESULT 2
AAV63468
ID   AAV63468 standard; cDNA; 1564 BP.
XX
AC   AAV63468;
XX
DT   26-JAN-1999  (first entry)
XX
DE   cDNA encoding G-protein coupled receptor (HFGAN72X) polypeptide.
XX
KW   G-protein coupled receptor; HFGAN72X; HIV infection; anorexia; cancer;
KW   bulimia; asthma; Parkinson's disease; acute heart failure;
KW   urinary retention; osteoporosis; angina pectoris; myocardial infarction;
KW   benign prostatic hypertrophy; neurological disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             154. .1431
FT                   /*tag=  a
FT                   /product= "HFGAN72X"
XX
PN   EP875566-A2.
XX
PD   04-NOV-1998.
XX
PF   27-OCT-1997;   97EP-00308563.
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XX
PR 30-APR-1997; 97US-00846704.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis CE;
XX
DR WPI; 1998-559432/48.
DR P-PSDB; AAW80456.
XX
PT New human G-protein coupled receptor HFGAN72X polypeptide and
PT polynucleotide - useful as diagnostic reagents and for treating e.g. HIV
PT infection, cancer and Parkinson's disease.
XX
PS Claim 3; Page 7; 24pp; English.
XX
CC The present sequence encodes a G-protein coupled receptor (HFGAN72X)
CC polypeptide. HFGAN72X polypeptides and polynucleotides are useful for
CC diagnosing diseases related to over or under expression of HFGAN72X
CC proteins by identifying mutations in the HFGAN72X gene using HFGAN72X
CC probes, or determining HFGAN72X protein or mRNA expression levels.
CC HFGAN72X polypeptides are also useful for screening for compounds which
CC affect activity of the protein. Diseases that can be treated with
CC HFGAN72X include HIV infections, pain, anorexia, cancers, bulimia,
CC asthma, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC myocardial infarction, ulcers, allergies, benign prostatic hypertrophy,
CC and psychotic and neurological disorders
XX
SQ Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

Query Match 99.7%; Score 1274.8; DB 2; Length 1564;
Best Local Similarity 99.8%; Pred. No. 1.9e-288;
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353
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Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1354 TCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy       1261 ACCACAGTGCTGCCCTGA 1278
             ||||||||||||||||||
Db       1414 ACCACAGTGCTGCCCTGA 1431


RESULT 3
AAV68514
ID   AAV68514 standard; cDNA; 1564 BP.
XX
AC   AAV68514;
XX
DT   29-JAN-1999  (first entry)
XX
DE   Nucleotide sequence of a probe HGS EST 554692.
XX
KW   Probe HGS EST 554692; G-protein coupled receptor family; HFGAN72Y;
KW   mutation; probe; agonist; antagonist; activation; inhibition;
KW   gene therapy; antibody; immune response; vaccine; HIV-1; HIV-2; cancer;
KW   anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
KW   hypotension; hypertension; urinary retention; osteoporosis;
KW   angina pectoris; myocardial infarction; ulcer; allergies;
KW   psychotic disorder; neurological disorder; gene mapping; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   EP875565-A2.
XX
PD   04-NOV-1998.
XX
PF   27-OCT-1997;   97EP-00308554.
XX
PR   30-APR-1997;   97US-00846705.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Bergsma DJ,  Ellis C;
XX
DR   WPI; 1998-570286/49.
XX
PT   New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -
PT   useful as diagnostic reagents and for prevention and treatment of HIV
PT   infections, cancer, osteoporosis and Parkinson's disease.
XX
PS   Example 1; Page 19-20; 22pp; English.
XX
CC   This is the nucleotide sequence of the probe HGS EST 554692 used in the
CC   method of the invention involving the G-protein coupled receptor,
CC   HFGAN72Y. Its polypeptides and polynucleotides are useful for diagnosing
CC   susceptibility to diseases by detecting mutations in the HFGAN72Y gene
CC   using probes containing the HFGAN72Y nucleotide sequence, and can
CC   diagnose diseases associated with HFGAN72Y imbalance by determining
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CC HFGAN72Y polypeptide or mRNA expression levels. Agonists/antagonists can
CC be used in treatment to activate/inhibit HFGAN72Y activity, in addition
CC to direct administration of antisense sequences to prevent expression, or
CC HFGAN72Y polypeptides to treat conditions associated with a lack HFGAN72Y
CC protein. Gene therapy may also be used to affect endogenous HFGAN72Y
CC polypeptide production. HFGAN72Y antibodies are useful for inducing an
CC immune response to immunise and prevent diseases, and for isolating
CC HFGAN72Y clones or purifying the polypeptides by affinity chromatography.
CC HFGAN72Y polypeptides can be administered directly or as a vaccine to
CC inoculate against diseases. Diseases diagnosed, prevented or treated
CC include HIV-1 or HIV-2 infections, pain, cancers, anorexia, bulimia,
CC asthma, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC myocardial infarction, ulcers; allergies, benign prostatic hypertrophy,
CC and psychotic and neurological disorders. The HFGAN72Y polypeptide is
CC also useful for mapping the gene to a chromosome, allowing gene
CC inheritance to be studied through linkage analysis
XX
SQ Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

Query Match 99.7%; Score 1274.8; DB 2; Length 1564;
Best Local Similarity 99.8%; Pred. No. 1.9e-288;
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
                ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 TCCTTGTAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy       1261 ACCACAGTGCTGCCCTGA 1278
                ||||||||||||||||||
Db       1414 ACCACAGTGCTGCCCTGA 1431
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RESULT 4

AAS17464
ID AAS17464 standard; DNA; 1564 BP.
XX
AC AAS17464;
XX
DT 25-FEB-2002 (first entry)
XX
DE Human G protein-coupled receptor HFGAN72 variant CDS.
XX
KW Human; G protein-coupled receptor; GPCR; HFGAN72; ds;
KW bacterial infection; fungal infection; protozoan infection;
KW viral infection; human immunodeficiency virus; HIV; cancer; diabetes;
KW Parkinson's disease; osteoporosis; myocardial infarction; ulcer; asthma;
KW allergy; angina pectoris; renal disease; depression; schizophrenia;
KW anorexia; obesity; Kallman's syndrome; hypothalamic disorder;
KW idiopathic hormone deficiency; gigantism; migraine; pain; lung disease;
KW burn; sleep disorder; jet lag; Huntington's disease; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 154. .1431
FT /*tag= a
FT /product= "HFGAN71X variant"
XX
PN US2001025031-A1.
XX
PD 27-SEP-2001.
XX
PF 06-APR-2001; 2001US-00828538.
XX
PR 08-JUN-1998; 98US-0088524P.
PR 22-JUL-1998; 98US-0093726P.
PR 08-JUN-1999; 99US-00328014.
XX
PA (ELLI/) ELLIS C E.
PA (KWOK/) KWOK C.
PA (BODS/) BODSWORTH N J.
PA (HALS/) HALSEY W.
PA (HORN/) HORN S V.
XX
PI Ellis CE, Kwok C, Bodsworth NJ, Halsey W, Horn SV;
XX
DR WPI; 2001-624968/72.
DR P-PSDB; AAU11188.
XX
PT Isolated HFGAN72 receptor useful for treatment of a patient having need
PT of HFGAN72 receptor and in the detection and treatment of disease, e.g.
PT infections such as bacterial, fungal, protozoan and viral infections and
PT cancers.
XX
PS Disclosure; Fig 5; 75pp; English.
XX
CC The invention relates to an isolated polypeptide, the HFGAN72 receptor or
CC its variant, encoded by the 8 exon sequences given in the specification.
CC HFGAN72 is a G protein-coupled receptor (GPCR). HFGAN72 is useful for the
CC treatment of a patient having need of HFGAN72 receptor where HFGAN72 is

CC administered by providing to the patient DNA encoding HFGAN72 and
CC expressing HFGAN72 in vivo (i.e by gene therapy). HFGAN72 is particularly
CC useful for applications in the detection and treatment of disease, e.g.
CC infections such as bacterial, fungal, protozoan and viral infections,
CC particularly infections caused by human immunodeficiency virus (HIV)-1 or
CC HIV-2, cancers, diabetes, Parkinson's disease, osteoporosis, myocardial
CC infarction, ulcers, asthma, allergies, angina pectoris, renal disease,
CC depression, schizophrenia, anorexia, obesity, Kallman's syndrome,
CC hypothalamic disorders, idiopathic hormone deficiency (e.g. gigantism),
CC migraine, pain, lung diseases, burns, sleep disorders, jet lag,
CC Huntington's disease and many other diseases and disorders given in the
CC specification. The present sequence is the coding sequence of an
CC alternative allele of the human HFGAN72 receptor
XX
SQ Sequence 1564 BP; 267 A; 514 C; 437 G; 346 T; 0 U; 0 Other;

Query Match 99.7%; Score 1274.8; DB 4; Length 1564;
Best Local Similarity 99.8%; Pred. No. 1.9e-288;
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGCGATTATCTG 273

Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy      421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy      541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy       1261 ACCACAGTGCTGCCCTGA 1278
                    ||||||||||||||||||
Db       1414 ACCACAGTGCTGCCCTGA 1431


RESULT 5
AAF32103
ID ' AAF32103 standard; cDNA; 1564 BP.
XX
AC   AAF32103;
```

XX
DT 10-APR-2001 (first entry)
XX
DE Human HFGAN72 receptor coding sequence SEQ ID NO: 12.
XX
KW Human; mouse; rat; Lig72A; Lig72B; neuropeptide receptor; HFGAN72;
KW truncation mutant; ligand; neurodegenerative disorder; pain;
KW eating disorder; behaviour disorder; mood disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200100787-A2.
XX
PD 04-JAN-2001.
XX
PF 22-JUN-2000; 2000WO-US017251.
XX
PR 25-JUN-1999; 99US-0141156P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Bingham S, Darker J, Liu W, Martin JD, Parsons AA, Patel SR;
XX
DR WPI; 2001-071483/08.
XX
PT Polynucleotides encoding Lig 72A polypeptides or their variants, which
PT are useful in the treatment of a disease or disorder associated with
PT pain, e.g. enhanced or exaggerated sensitivity to pain, hyperalgesia,
PT neuropathic pain and back pain.
XX
PS Disclosure; Fig 6; 101pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC human, mouse and rat HFGAN receptor ligand Lig72A. It also provides
CC truncated mutant versions. These, and their agonists and antagonists, are
CC all useful in the treatment of eating, neurodegenerative, behaviour,
CC mood, sexual, hormonal and sleep disorders, pain, depression, epilepsy
CC and acute inflammatory conditions
XX
SQ Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

Query Match 99.7%; Score 1274.8; DB 4; Length 1564;
Best Local Similarity 99.8%; Pred. No. 1.9e-288;
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333
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Qy       181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db       334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy       421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db       634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy       541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy       601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy       781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       934 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173
```

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Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
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Db       1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1354 TCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy       1261 ACCACAGTGCTGCCCTGA 1278
             ||||||||||||||||||
Db       1414 ACCACAGTGCTGCCCTGA 1431
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```
RESULT 6
ABA96021
ID   ABA96021 standard; cDNA; 1564 BP.
XX
AC   ABA96021;
XX
DT   12-MAR-2002  (first entry)
XX
DE   HGS EST 554692.
XX
KW   G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;
KW   nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;
KW   infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;
KW   cardiac disease; urinary retention; asthma; allergy; psychotic disorder;
KW   benign prostatic hypertrophy; neurological disorder; anxiety; delirium;
KW   schizophrenia; manic depression; dementia; mental retardation; EST;
KW   dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2;
KW   HGS EST 554692; expressed sequence tag; probe; ss.
XX
OS   Homo sapiens.
XX
PN   EP1156110-A2.
XX
PD   21-NOV-2001.
XX
PF   27-OCT-1997; 2001EP-00203010.
XX
PR   30-APR-1997;   97US-00846705.
PR   27-OCT-1997;   97EP-00308554.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Bergsma DJ,  Ellis CE;
XX
DR   WPI; 2002-084320/12.
XX
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PT New polynucleotide encoding a G-protein coupled receptor designated
PT HFGAN72Y is useful to diagnose and treat associated diseases including
PT cancer, infection, cardiac disease and psychotic and neurological
PT disorders.
XX
PS Example 1; Page 19-20; 22pp; English.
XX
CC The sequence represents HGS EST 554692. The sequence was used in the
CC invention as a probe to screen a human genomic placenta phage library.
CC The invention relates to a novel isolated polynucleotide encoding
CC HFGAN72Y polypeptide. The polypeptide of the invention has cytostatic,
CC cardiant, analgesic, tranquillising, nootropic, neuroprotective, and anti
CC -asthmatic activity. The HFGAN72Y has a use in gene therapy. The HFGAN72Y
CC polynucleotide or an HFGAN72Y polypeptide agonist are used to treat a
CC subject in need of enhanced HFGAN72Y activity or expression. An HFGAN72Y
CC antagonist or competitor, or nucleic acid which inhibits HFGAN72Y
CC expression is used to treat a subject in need of decreased HFGAN72Y
CC activity or expression. HFGAN72Y-associated diseases include infections,
CC particularly by HIV-1 or HIV-2, pain, anorexia, bulimia, Parkinson's
CC disease, cardiac diseases, cancers, ulcers, urinary retention, asthma,
CC allergies, benign prostatic hypertrophy, and psychotic and neurological
CC disorders including anxiety, schizophrenia, manic depression, delirium,
CC dementia, severe mental retardation and dyskinesias such as Huntington's
CC disease and Tourette's syndrome
XX
SQ Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

Query Match 99.7%; Score 1274.8; DB 6; Length 1564;
Best Local Similarity 99.8%; Pred. No. 1.9e-288;
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
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Db       1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 TCCTTGTAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413
```

```
Qy       1261 ACCACAGTGCTGCCCTGA 1278
              ||||||||||||||||||
Db       1414 ACCACAGTGCTGCCCTGA 1431


RESULT 7
AAI64173
ID   AAI64173 standard; cDNA; 1564 BP.
XX
AC   AAI64173;
XX
DT   22-JAN-2002  (first entry)
XX
DE   HFGAN72X G coupled receptor polypeptide partial sequence.
XX
KW   Antibacterial; fungicide; virucide; protozoacide; anti-HIV; analgesic;
KW   cytostatic; nootropic; antiparkinsonian; cardiant; antiulcer;
KW   antiasthmatic; tranquiliser; neuroleptic; antidepressant; anticonvulsant;
KW   osteopathic; HIV infection; pain; cancer; anorexia; bulimia;
KW   Parkinson's disease; acute heart failure; hypotension; hypertension;
KW   urinary retention; osteoporosis; angina pectoris; probe;
KW   myocardial infarction; ulcers; asthma; allergy; delirium; dementia;
KW   benign prostatic hypertrophy; anxiety; schizophrenia; manic depression;
KW   dyskinesia; G coupled receptor; HFGAN72X; 7 transmembrane receptor; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             154. .1362
FT                   /*tag=  a
FT                   /partial
FT                   /product= "HFGAN72X protein"
FT                   /note= "The specification states that this is a partial
FT                   sequence even though it contains start and stop codons;
FT                   HFGAN72X is a G coupled receptor polypeptide"
FT                   /transl_except= (pos:991. .993, aa:Ala)
XX
PN   EP1154019-A2.
XX
PD   14-NOV-2001.
XX
PF   27-OCT-1997; 2001EP-00203008.
XX
PR   30-APR-1997;   97US-00846704.
PR   27-OCT-1997;   97EP-00308563.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Bergsma DJ,  Ellis CE;
XX
DR   WPI; 2002-012659/02.
DR   P-PSDB; AAG78346.
XX
PT   Nucleic acid encoding the HFGAN72X receptor, useful for diagnosis and
PT   treatment of e.g. infections, cancer, anorexia, bulimia, Parkinson's
PT   disease, and acute heart failure.
```

XX
PS Example 3; Page 9; 24pp; English.
XX
CC The present sequence is that of a known partial nucleotide sequence
CC encoding a HFGAN72X polypeptide (AAG78346) used as a probe to identify
CC the HFGAN72X gene (AAI64173). The specification describes a newly
CC isolated polynucleotide encoding a human HFGAN72X G coupled receptor
CC polypeptide. The protein of the invention has antibacterial, fungicide,
CC virucide, protozoacide, anti-HIV, cardiant, analgesic, cytostatic,
CC nootropic, antiparkinsonian, antiulcer, antiasthmatic, tranquiliser,
CC neuroleptic, antidepressant, anticonvulsant and osteopathic activities.
CC HFGAN72X polynucleotides (PNs) are used to express HFGAN72X in vivo, to
CC treat diseases requiring increased activity or expression of HFGAN72X;
CC for recombinant production of HFGAN72X; diagnose diseases by detecting
CC mutations in genomic sequences and in chromosome identification and
CC mapping. HFGAN72X polypeptides are used to raise specific antibodies; as
CC therapeutic agents; to identify HFGAN72X protein-expressing clones; to
CC purify HFGAN72X proteins; in vaccines. Cells transformed with HFGAN72X
CC PNs are used to identify (ant)agonists of HFGAN72X, useful
CC therapeutically. Nucleic acids that inhibit expression of HFGAN72X and
CC polypeptides that compete with ligands for binding to HFGAN72X proteins
CC are also useful therapeutically and diagnostically. HFGAN72X-related
CC diseases include infections (bacterial, viral, fungal or protozoal,
CC particularly HIV-1 or -2); pain; cancer; anorexia; bulimia; Parkinson's
CC disease; acute heart failure; hypotension; hypertension; urinary
CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
CC asthma; allergy; benign prostatic hypertrophy; anxiety; schizophrenia;
CC manic depression; delirium; dementia; severe mental retardation and
CC dyskinesias
XX
SQ Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

Query Match 99.7%; Score 1274.8; DB 6; Length 1564;
Best Local Similarity 99.8%; Pred. No. 1.9e-288;
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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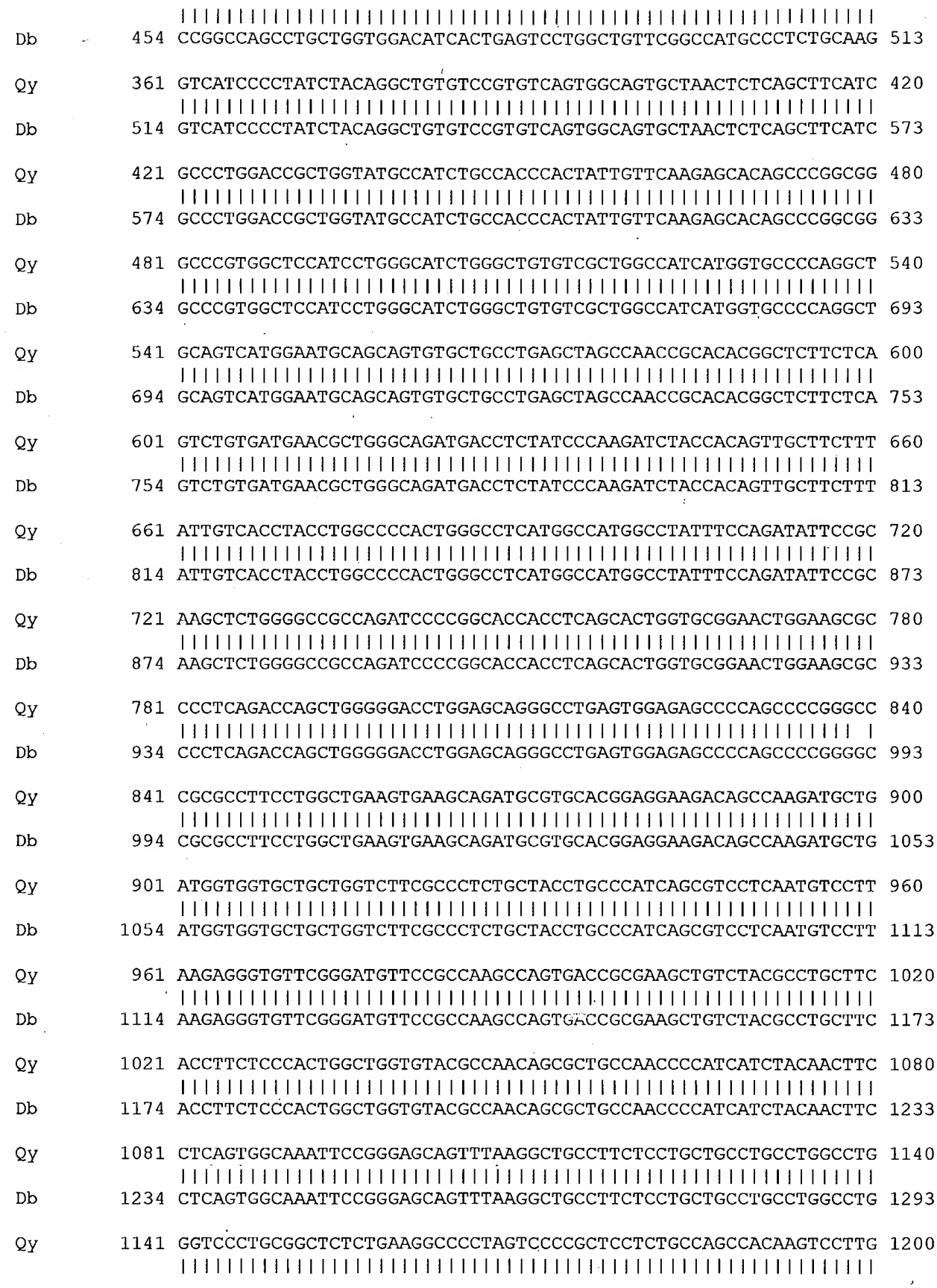

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Db       1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1354 TCCTTGTAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy       1261 ACCACAGTGCTGCCCTGA 1278
              ||||||||||||||||||
Db       1414 ACCACAGTGCTGCCCTGA 1431


RESULT 8
AAI64172
ID   AAI64172 standard; cDNA; 1564 BP.
XX
AC   AAI64172;
XX
DT   22-JAN-2002  (first entry)
XX
DE   Human HFGAN72X G coupled receptor polypeptide cDNA.
XX
KW   Antibacterial; fungicide; virucide; protozoacide; anti-HIV; analgesic;
KW   cytostatic; nootropic; antiparkinsonian; cardiant; antiulcer;
KW   antiasthmatic; tranquiliser; neuroleptic; antidepressant; anticonvulsant;
KW   osteopathic; HIV infection; pain; cancer; anorexia; bulimia;
KW   Parkinson's disease; acute heart failure; hypotension; hypertension;
KW   urinary retention; osteoporosis; angina pectoris; myocardial infarction;
KW   ulcers; asthma; allergy; delirium; dementia;
KW   benign prostatic hypertrophy; anxiety; schizophrenia; manic depression;
KW   dyskinesia; G coupled receptor; HFGAN72X; 7 transmembrane receptor; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             154. .1431
FT                   /*tag=  a
FT                   /product= "HFGAN72X protein"
FT                   /note= "G coupled receptor polypeptide"
XX
PN   EP1154019-A2.
XX
PD   14-NOV-2001.
XX
PF   27-OCT-1997; 2001EP-00203008.
XX
PR   30-APR-1997;   97US-00846704.
PR   27-OCT-1997;   97EP-00308563.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Bergsma DJ,  Ellis CE;
XX
DR   WPI; 2002-012659/02.
DR   P-PSDB; AAG78345.
XX
PT   Nucleic acid encoding the HFGAN72X receptor, useful for diagnosis and
PT   treatment of e.g. infections, cancer, anorexia, bulimia, Parkinson's
```

PT disease, and acute heart failure.
XX
PS Claim 3; Page 7; 24pp; English.
XX
CC The present sequence is that of a cDNA encoding a HFGAN72X polypeptide
CC (AAG78345). The specification describes a newly isolated polynucleotide
CC encoding a HFGAN72X G coupled receptor polypeptide. The protein of the
CC invention has antibacterial, fungicide, virucide, protozoacide, anti-HIV,
CC cardiant, analgesic, cytostatic, nootropic, antiparkinsonian, antiulcer,
CC antiasthmatic, tranquiliser, neuroleptic, antidepressant, anticonvulsant
CC and osteopathic activities. HFGAN72X polynucleotides (PNs) are used to
CC express HFGAN72X in vivo, to treat diseases requiring increased activity
CC or expression of HFGAN72X; for recombinant production of HFGAN72X;
CC diagnose diseases (or susceptibility to them) by detecting mutations in
CC genomic sequences and in chromosome identification and mapping. HFGAN72X
CC polypeptides are used to raise specific antibodies; as therapeutic agents
CC ; to identify HFGAN72X protein-expressing clones; to purify HFGAN72X
CC proteins; in vaccines. Cells transformed with HFGAN72X PNs are used to
CC identify (ant)agonists of HFGAN72X, useful therapeutically. Nucleic acids
CC that inhibit expression of HFGAN72X and polypeptides that compete with
CC ligands for binding to HFGAN72X proteins are also useful therapeutically
CC and diagnostically. HFGAN72X-related diseases include infections
CC (bacterial, viral, fungal or protozoal, particularly HIV-1 or -2); pain;
CC cancer; anorexia; bulimia; Parkinson's disease; acute heart failure;
CC hypotension; hypertension; urinary retention; osteoporosis; angina
CC pectoris; myocardial infarction; ulcers; asthma; allergy; benign
CC prostatic hypertrophy; anxiety; schizophrenia; manic depression; delirium
CC ; dementia; severe mental retardation and dyskinesias
XX
SQ Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

Query Match 99.7%; Score 1274.8; DB 6; Length 1564;
Best Local Similarity 99.8%; Pred. No. 1.9e-288;
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
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Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
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Db       1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353
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Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
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Db       1354 TCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy       1261 ACCACAGTGCTGCCCTGA 1278
             ||||||||||||||||||
Db       1414 ACCACAGTGCTGCCCTGA 1431
```

RESULT 9
ABZ42789
ID ABZ42789 standard; DNA; 1564 BP.
XX
AC ABZ42789;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human orexin receptor 1 nucleotide SEQ ID NO:367.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
DR P-PSDB; ABP81941.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a)

CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 1564 BP; 268 A; 513 C; 436 G; 347 T; 0 U; 0 Other;

Query Match 99.7%; Score 1274.8; DB 7; Length 1564;
Best Local Similarity 99.8%; Pred. No. 1.9e-288;
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
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Db       1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1354 TCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413
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Qy       1261 ACCACAGTGCTGCCCTGA 1278
              ||||||||||||||||||
Db       1414 ACCACAGTGCTGCCCTGA 1431


RESULT 10
ABI98014
ID   ABI98014 standard; cDNA; 1278 BP.
XX
AC   ABI98014;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Non-endogenous human GPCR cDNA, SEQ ID NO: 548.
XX
KW   Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KW   constitutively activated GPCR; agonist; disease; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200177172-A2.
XX
PD   18-OCT-2001.
XX
PF   05-APR-2001; 2001WO-US011098.
XX
PR   07-APR-2000; 2000US-0195747P.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Lehmann-Bruinsma K,  Liaw CW,  Lin I;
XX
DR   WPI; 2001-648759/74.
DR   P-PSDB; ABB56378.
XX
PT   Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT   disease treatment, comprises contacting candidate compounds with versions
PT   of GPCRs.
XX
PS   Example 2; Page 349-350; 394pp; English.
XX
CC   The invention relates to G protein-coupled receptors (GPCRs) for which
CC   the endogenous ligand has been identified. Non-endogenous constitutively
CC   activated versions of known GPCRs are used in the invention for the
CC   direct identification of candidate compounds as receptor agonists,
CC   inverse agonists or partial agonists. Such agonists are useful as
CC   therapeutic agents for diseases or disorders associated with GPCRs. The
CC   present sequence encodes a non-endogenous version of a known human GPCR
XX
SQ   Sequence 1278 BP; 224 A; 423 C; 346 G; 285 T; 0 U; 0 Other;

  Query Match             99.4%;  Score 1270;  DB 5;  Length 1278;
  Best Local Similarity   99.6%;  Pred. No. 2.3e-287;
  Matches 1273;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;
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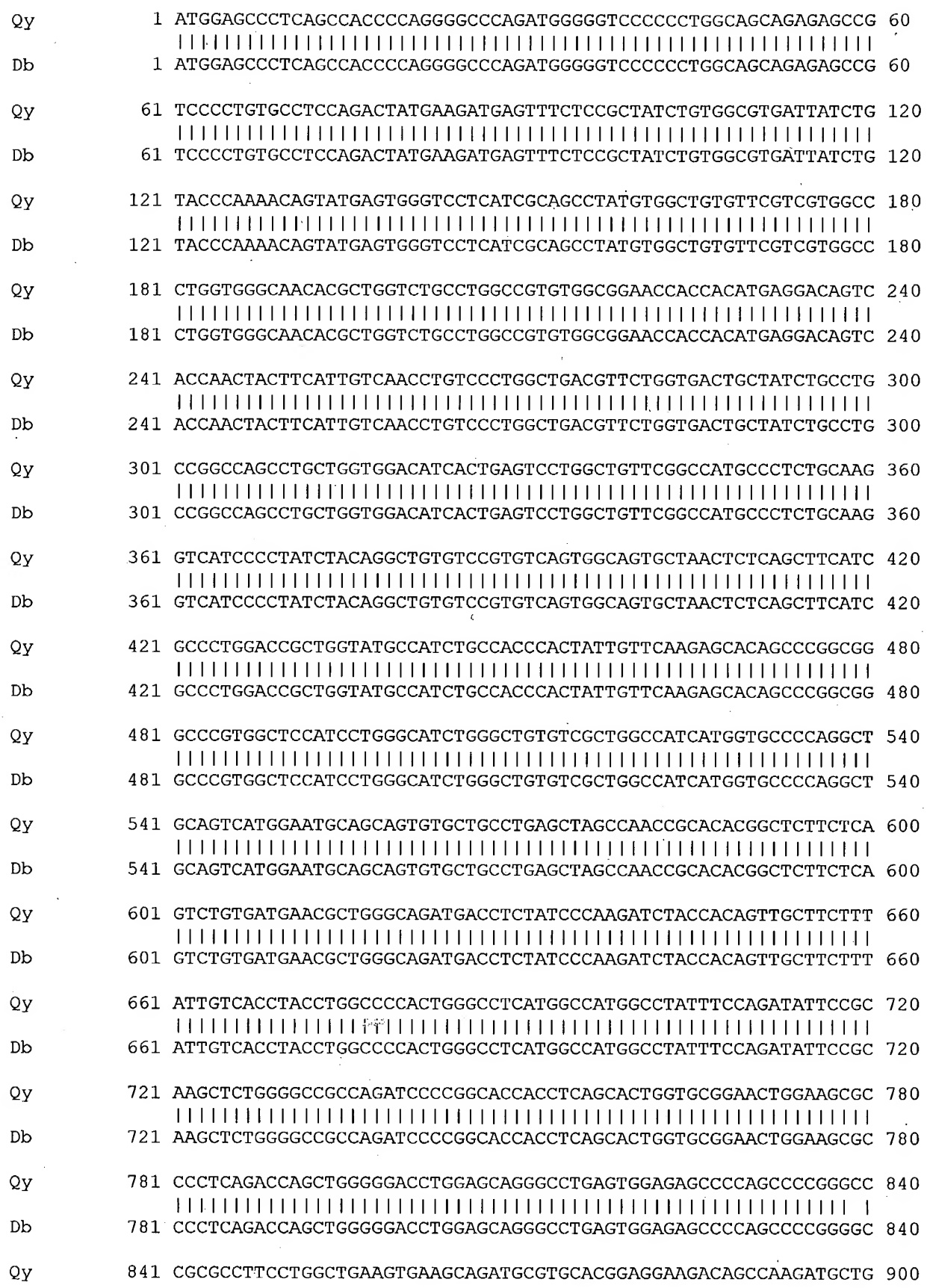
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Db 1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Qy 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
Db 421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
Db 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
Qy 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
Db 541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
Qy 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
Db 601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
Qy 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
Db 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db          841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAAAAAAGATGCTG 900

Qy          901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy          961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy         1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy         1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140

Qy         1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200

Qy         1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
                |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db         1201 TCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260

Qy         1261 ACCACAGTGCTGCCCTGA 1278
                ||||||||||||||||||
Db         1261 ACCACAGTGCTGCCCTGA 1278
```

RESULT 11

AAD09335

```
ID   AAD09335 standard; cDNA; 1278 BP.
XX
AC   AAD09335;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Cynomolgous Monkey Orexin 1 Receptor cDNA.
XX
KW   Cynomolgous monkey; Orexin 1 Receptor; 7 Transmembrane Receptor family;
KW   7TM; gene therapy; vaccine; microbial infection; HIV-1; HIV-2; pain;
KW   cancer; diabetes; obesity; anorexia; bulimia; urinary retention;
KW   Parkinson's disease; acute heart failure; hypotension; hypertension;
KW   osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer;
KW   asthma; allergy; benign prostatic hypertrophy; migraine; vomiting;
KW   psychotic disorder; neurological disorder; anxiety; schizophrenia;
KW   manic depression; depression; delirium; dementia; mental retardation;
KW   dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; ss.
XX
OS   Macaca fascicularis.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1278
FT                   /*tag=  a
```

FT   /product= "Orexin 1 Receptor"
XX
PN   WO200140259-A2.
XX
PD   07-JUN-2001.
XX
PF   04-DEC-2000; 2000WO-US032849.
XX
PR   02-DEC-1999;   99US-0168553P.
PR   28-NOV-2000; 2000US-00723781.
XX
PA   (SMIK) SMITHKLINE BEECHAM CORP.
PA   (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI   Ellis CE;
XX
DR   WPI; 2001-408276/43.
DR   P-PSDB; AAE04740.
XX
PT   Novel Cynomolgous Monkey Orexin 1 Receptor polypeptides, for treating
PT   infections, pain, cancer, diabetes, obesity, asthma, schizophrenia,
PT   hypertension, urinary retention, Parkinson's disease and stroke.
XX
PS   Claim 1; Page 28; 33pp; English.
XX
CC   The present sequence is a cDNA encoding Cynomolgous Monkey Orexin 1
CC   Receptor which is structurally related to members of 7 Transmembrane
CC   Receptor (7TM) family. The Orexin 1 Receptor polypeptide and
CC   polynucleotide are useful for treating bacterial, fungal, protozoan and
CC   viral infections, particularly infections caused by HIV-1 or HIV-2, pain,
CC   cancer, diabetes, obesity, anorexia, bulimia, Parkinson's disease, acute
CC   heart failure, hypotension, hypertension, urinary retention,
CC   osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers,
CC   asthma, allergies, benign prostatic hypertrophy, migraine, vomiting,
CC   psychotic and neurological disorders including anxiety, schizophrenia,
CC   manic depression, depression, delirium, dementia and severe mental
CC   retardation, and dyskinesias, such as Huntington's disease or Gilles de
CC   la Tourette's syndrome. The polypeptide is also useful for structure-
CC   based design of its agonist, antagonist or inhibitor. The polynucleotide
CC   is useful for chromosome localisation studies and in gene therapy. The
CC   Orexin 1 Receptor polypeptide and polynucleotide are also useful as
CC   vaccines
XX
SQ   Sequence 1278 BP; 219 A; 433 C; 346 G; 280 T; 0 U; 0 Other;

  Query Match   95.9%; Score 1225.2; DB 4; Length 1278;
  Best Local Similarity   97.4%; Pred. No. 7.1e-277;
  Matches 1245; Conservative   0; Mismatches   33; Indels   0; Gaps   0;

Qy   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||| |||||||| |||||||||| |||||
Db   1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGCGGGTCCCCACTGGCAGCAGGGAGCCA 60

Qy   61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              |||||||||||||||||||||||| |||||||||||| |||||||| |||||||||
Db   61 TCCCCTGTGCCTCCAGACTATGAAGACGAGTTTCTCCGCTACCTGTGGCGCGATTATCTG 120

```
Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||| ||||||||||||||||||||||||||||||||||| ||||||||
Db        121 TACCCAAAACAGTACGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCCTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||| |||||||||||||||||||||||||||| ||||| |||||||||
Db        241 ACCAACTACTTCATCGTCAACCTGTCCCTGGCTGACGTTCTGGTAACTGCCATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              |||| ||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        301 CCGGTCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCTCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              |||||||||||||||||| |||||||||||||||||||| ||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCCGTGTCCGTGTCAGTGGCAGTGCTGACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCTGTCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCCGAGCTAGCCAACCGCACACGGCTCTTCTCG 600

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTATATCCCAAGATCTACCACAGTTGCTTCTTC 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              |||||||||||||||||| |||||||||||||||||||||||| ||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATTCCCGGCACCACCTCAGCACTGGTGCGAAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGACAGCCCCAGCCCCGGGCC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCGCGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||| |||||||||||||||||||||| ||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTTGCCCTCTGCTACCTGCCCATCAGTGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
                |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGTGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCCG 1140

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
                || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGCCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200

Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
                |||||||||||||||||||||||||||||| |||||||||| ||||||||||||||||||
Db       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAACTCTCTGAGCACGTGGTGCTCACCAGCGTC 1260

Qy       1261 ACCACAGTGCTGCCCTGA 1278
                ||||||||||||||||||
Db       1261 ACCACAGTGCTGCCCTGA 1278
```

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RESULT 12
AAT42826
ID   AAT42826 standard; cDNA; 1209 BP.
XX
AC   AAT42826;
XX
DT   22-FEB-1997  (first entry)
XX
DE   Neuropeptide receptor gene.
XX
KW   Human; neuropeptide receptor; drug screening; receptor-agonist;
KW   receptor-antagonist; anorectic; antitumour; anticholesterolemic;
KW   neuroprotective; anticonvulsant; hypotensive; sedative; diagnostic;
KW   gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     complement(1. .18)
FT                   /*tag=  a
FT                   /note= "Binds primer AAT42829"
FT   misc_difference 151. .153
FT                   /*tag=  b
FT                   /codon= seq:CCA, aa:Ala
FT   primer_bind     complement(1190. .1192)
FT                   /*tag=  c
FT                   /note= "Binds primers AAT42830 and AAT42832"
XX
PN   WO9634877-A1.
XX
PD   07-NOV-1996.
XX
PF   05-MAY-1995;   95WO-US005616.
```

XX
PR 05-MAY-1995; 95WO-US005616.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Soppet DR, Li Y, Rosen CA;
XX
DR WPI; 1996-506094/50.
DR P-PSDB; AAW06124.
XX
PT Human neuro-peptide receptor polypeptide(s) - used to identify
PT antagonists and agonists to such polypeptide(s), e.g. in the treatment of
PT obesity, Alzheimer's disease, epilepsy, etc.
XX
PS Claim 6; Page 48-49; 77pp; English.
XX
CC The sequence encodes a human neuropeptide receptor, and has been mapped
CC to human chromosome 1q31-34. The sequence has been isolated from a human
CC adult hypothalamus cDNA library, and is structurally related to the G-
CC protein-coupled receptor family. Splice variants are given in AAT42827-
CC 28. The sequence may be amplified by PCR with e.g. primers AAT42829-34
CC for expression in a host cell. The recombinant receptor may be used in a
CC drug screening assay for isolation of receptor-agonists and -antagonists,
CC which may be used as anorectic, antitumour, anticholesterolemic,
CC neuroprotective, anticonvulsant, hypotensive or sedative drugs, etc. The
CC DNA may also be used in genetic disease diagnosis or gene therapy. The
CC receptor and its corresponding antibody may also be used in therapy and
CC diagnosis
XX
SQ Sequence 1209 BP; 206 A; 402 C; 330 G; 271 T; 0 U; 0 Other;

Query Match 94.1%; Score 1202.6; DB 2; Length 1209;
Best Local Similarity 99.7%; Pred. No. 1.4e-271;
Matches 1205; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCCCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
```

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Qy       1201 TCCTTGCAG 1209
              |||||| ||
Db       1201 TCCTTGTAG 1209


RESULT 13
AAV68512
ID   AAV68512 standard; cDNA; 1133 BP.
XX
AC   AAV68512;
XX
DT   29-JAN-1999  (first entry)
XX
DE   Nucleotide sequence of HGS EST 557082.
XX
KW   HGS EST 557082; G-protein coupled receptor family; HFGAN72Y; mutation;
KW   probe; agonist; antagonist; activation; inhibition; gene therapy;
KW   antibody; immune response; vaccine; HIV-1; HIV-2; cancer; anorexia;
KW   bulimia; asthma; Parkinson's disease; acute heart failure; hypotension;
KW   hypertension; urinary retention; osteoporosis; angina pectoris;
KW   myocardial infarction; ulcer; allergies; psychotic disorder;
KW   neurological disorder; gene mapping; ss.
XX
OS   Homo sapiens.
XX
PN   EP875565-A2.
XX
PD   04-NOV-1998.
XX
PF   27-OCT-1997;   97EP-00308554.
XX
PR   30-APR-1997;   97US-00846705.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Bergsma DJ,  Ellis C;
XX
DR   WPI; 1998-570286/49.
XX
PT   New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -
PT   useful as diagnostic reagents and for prevention and treatment of HIV
PT   infections, cancer, osteoporosis and Parkinson's disease.
XX
PS   Example 1; Page 18-19; 22pp; English.
XX
CC   This is the nucleotide sequence of the HGS EST 557082 used in the method
CC   of the invention involving the G-protein coupled receptor, HFGAN72Y. Its
CC   polypeptides and polynucleotides are useful for diagnosing susceptibility
CC   to diseases by detecting mutations in the HFGAN72Y gene using probes
CC   containing the HFGAN72Y nucleotide sequence, and can diagnose diseases
CC   associated with HFGAN72Y imbalance by determining HFGAN72Y polypeptide or
CC   mRNA expression levels. Agonists/antagonists can be used in treatment to
CC   activate/inhibit HFGAN72Y activity, in addition to direct administration
CC   of antisense sequences to prevent expression, or HFGAN72Y polypeptides to
CC   treat conditions associated with a lack HFGAN72Y protein. Gene therapy
CC   may also be used to affect endogenous HFGAN72Y polypeptide production.
```

CC HFGAN72Y antibodies are useful for inducing an immune response to
CC immunise and prevent diseases, and for isolating HFGAN72Y clones or
CC purifying the polypeptides by affinity chromatography. HFGAN72Y
CC polypeptides can be administered directly or as a vaccine to inoculate
CC against diseases. Diseases diagnosed, prevented or treated include HIV-1
CC or HIV-2 infections, pain, cancers, anorexia, bulimia, asthma,
CC Parkinson's disease, acute heart failure, hypotension, hypertension,
CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,
CC ulcers; allergies, benign prostatic hypertrophy, and psychotic and
CC neurological disorders. The HFGAN72Y polypeptide is also useful for
CC mapping the gene to a chromosome, allowing gene inheritance to be studied
CC through linkage analysis
XX
SQ Sequence 1133 BP; 202 A; 366 C; 314 G; 251 T; 0 U; 0 Other;

Query Match 85.0%; Score 1086.4; DB 2; Length 1133;
Best Local Similarity 99.9%; Pred. No. 2.1e-244;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
              ||||||||
Db       1081 CTCAGTGG 1088
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RESULT 14
ABA96020
ID ABA96020 standard; cDNA; 1133 BP.
XX
AC ABA96020;
XX
DT 12-MAR-2002 (first entry)
XX
DE HGS EST 557082.
XX
KW G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;
KW nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;
KW infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;
KW cardiac disease; urinary retention; asthma; allergy; psychotic disorder;
KW benign prostatic hypertrophy; neurological disorder; anxiety; delirium;
KW schizophrenia; manic depression; dementia; mental retardation; EST;
KW dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2;
KW HGS EST 557082; expressed sequence tag; ss.

XX
OS Homo sapiens.
XX
PN EP1156110-A2.
XX
PD 21-NOV-2001.
XX
PF 27-OCT-1997; 2001EP-00203010.
XX
PR 30-APR-1997; 97US-00846705.
PR 27-OCT-1997; 97EP-00308554.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis CE;
XX
DR WPI; 2002-084320/12.
XX
PT New polynucleotide encoding a G-protein coupled receptor designated
PT HFGAN72Y is useful to diagnose and treat associated diseases including
PT cancer, infection, cardiac disease and psychotic and neurological
PT disorders.
XX
PS Example 1; Page 18-19; 22pp; English.
XX
CC The sequence represents HGS EST 557082. The invention relates to a novel
CC isolated polynucleotide encoding HFGAN72Y polypeptide. The polypeptide of
CC the invention has cytostatic, cardiant, analgesic, tranquillising,
CC nootropic, neuroprotective, and anti-asthmatic activity. The HFGAN72Y has
CC a use in gene therapy. The HFGAN72Y polynucleotide or an HFGAN72Y
CC polypeptide agonist are used to treat a subject in need of enhanced
CC HFGAN72Y activity or expression. An HFGAN72Y antagonist or competitor, or
CC nucleic acid which inhibits HFGAN72Y expression is used to treat a
CC subject in need of decreased HFGAN72Y activity or expression. HFGAN72Y-
CC associated diseases include infections, particularly by HIV-1 or HIV-2,
CC pain, anorexia, bulimia, Parkinson's disease, cardiac diseases, cancers,
CC ulcers, urinary retention, asthma, allergies, benign prostatic
CC hypertrophy, and psychotic and neurological disorders including anxiety,
CC schizophrenia, manic depression, delirium, dementia, severe mental
CC retardation and dyskinesias such as Huntington's disease and Tourette's
CC syndrome
XX
SQ Sequence 1133 BP; 202 A; 366 C; 314 G; 251 T; 0 U; 0 Other;

Query Match 85.0%; Score 1086.4; DB 6; Length 1133;
Best Local Similarity 99.9%; Pred. No. 2.1e-244;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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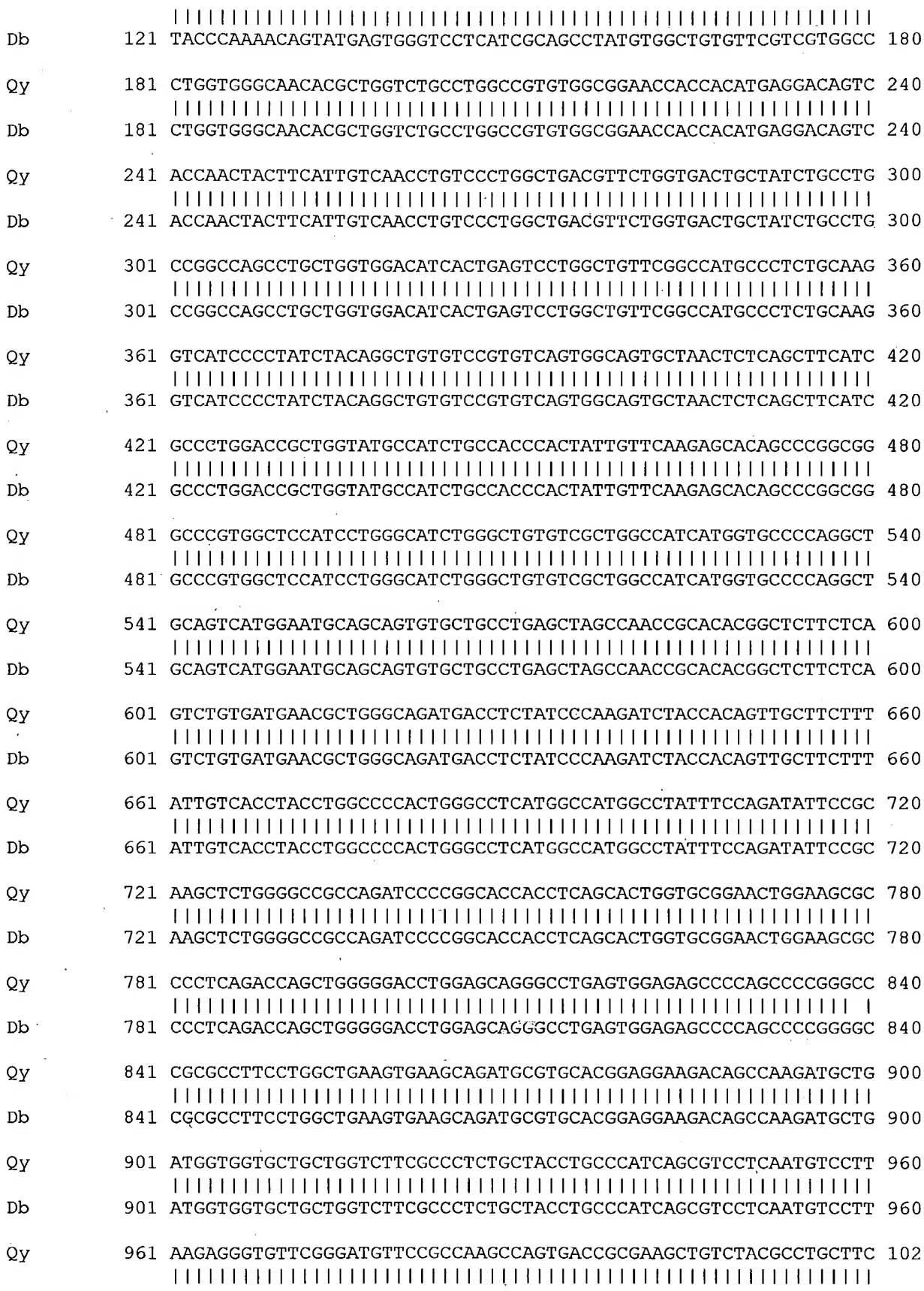

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Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
              ||||||||
Db       1081 CTCAGTGG 1088


RESULT 15
AAV68511
ID   AAV68511 standard; cDNA; 1170 BP.
XX
AC   AAV68511;
XX
DT   29-JAN-1999  (first entry)
XX
DE   Nucleotide sequence of HFGAN72Y a G-protein coupled receptor.
XX
KW   G-protein coupled receptor family; HFGAN72Y; mutation; probe; agonist;
KW   antagonist; activation; inhibition; gene therapy; antibody;
KW   immune response; vaccine; HIV-1; HIV-2; cancer; anorexia; bulimia;
KW   asthma; Parkinson's disease; acute heart failure; hypotension;
KW   hypertension; urinary retention; osteoporosis; angina pectoris;
KW   myocardial infarction; ulcer; allergies; psychotic disorder;
KW   neurological disorder; gene mapping; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1170
FT                   /*tag=  a
FT                   /product= "HFGAN72Y protein"
XX
PN   EP875565-A2.
XX
PD   04-NOV-1998.
XX
PF   27-OCT-1997;   97EP-00308554.
XX
PR   30-APR-1997;   97US-00846705.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Bergsma DJ,  Ellis C;
XX
DR   WPI; 1998-570286/49.
DR   P-PSDB; AAW80805.
XX
PT   New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -
PT   useful as diagnostic reagents and for prevention and treatment of HIV
PT   infections, cancer, osteoporosis and Parkinson's disease.
XX
PS   Claim 3; Page 7; 22pp; English.
XX
```

CC This is the nucleotide sequence of the G-protein coupled receptor,
CC HFGAN72Y used in the method of the invention. HFGAN72Y polypeptides and
CC polynucleotides are useful for diagnosing susceptibility to diseases by
CC detecting mutations in the HFGAN72Y gene using probes containing the
CC HFGAN72Y nucleotide sequence, and can diagnose diseases associated with
CC HFGAN72Y imbalance by determining HFGAN72Y polypeptide or mRNA expression
CC levels. Agonists/antagonists can be used in treatment to activate/inhibit
CC HFGAN72Y activity, in addition to direct administration of antisense
CC sequences to prevent expression, or HFGAN72Y polypeptides to treat
CC conditions associated with a lack HFGAN72Y protein. Gene therapy may also
CC be used to affect endogenous HFGAN72Y polypeptide production. HFGAN72Y
CC antibodies are useful for inducing an immune response to immunise and
CC prevent diseases, and for isolating HFGAN72Y clones or purifying the
CC polypeptides by affinity chromatography. HFGAN72Y polypeptides can be
CC administered directly or as a vaccine to inoculate against diseases.
CC Diseases diagnosed, prevented or treated include HIV-1 or HIV-2
CC infections, pain, cancers, anorexia, bulimia, asthma, Parkinson's
CC disease, acute heart failure, hypotension, hypertension, urinary
CC retention, osteoporosis, angina pectoris, myocardial infarction, ulcers;
CC allergies, benign prostatic hypertrophy, and psychotic and neurological
CC disorders. The HFGAN72Y polypeptide is also useful for mapping the gene
CC to a chromosome, allowing gene inheritance to be studied through linkage
CC analysis
XX
SQ Sequence 1170 BP; 208 A; 381 C; 322 G; 259 T; 0 U; 0 Other;

Query Match 85.0%; Score 1086.4; DB 2; Length 1170;
Best Local Similarity 99.9%; Pred. No. 2.1e-244;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Searched: 682709 seqs, 277475446 residues

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Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1274.8	99.7	1564	2	US-08-846-705-4	Sequence 4, Appli
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3	1274.8	99.7	1564	3	US-08-846-704-3	Sequence 3, Appli
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5	1201	94.0	1209	5	PCT-US95-05616-1	Sequence 1, Appli
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9	1083.2	84.8	1116	4	US-08-462-509B-5	Sequence 5, Appli
10	1083.2	84.8	1133	5	PCT-US95-05616-5	Sequence 5, Appli
11	1077.8	84.3	1110	5	PCT-US95-05616-3	Sequence 3, Appli

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21	119	9.3	1110	3	US-08-513-974B-31	Sequence 31, Appl
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ALIGNMENTS

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RESULT 1
US-08-846-705-4
; Sequence 4, Application US/08846705
; Patent No. 5935814
;  GENERAL INFORMATION:
;    APPLICANT:  BERGSMA, DERK J.
;    APPLICANT:  ELLIS, CATHERINE E
;    TITLE OF INVENTION:  NOVEL G-PROTEIN COUPLED
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
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;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/846,705
;       FILING DATE:  30-APR-1997
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  PRESTIA, PAUL F
;       REGISTRATION NUMBER:  23,031
;       REFERENCE/DOCKET NUMBER:  GH-70003
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  610-407-0700
;       TELEFAX:  610-407-0701
;       TELEX:  846169
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1564 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-846-705-4

  Query Match             99.7%;  Score 1274.8;  DB 2;  Length 1564;
  Best Local Similarity   99.8%;  Pred. No. 3.2e-287;
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Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
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Db       1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
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Db       1354 TCCTTGTAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413
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Qy       1261 ACCACAGTGCTGCCCTGA 1278
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Db       1414 ACCACAGTGCTGCCCTGA 1431


RESULT 2
US-08-846-704-1
; Sequence 1, Application US/08846704
; Patent No. 6020157
;  GENERAL INFORMATION:
;    APPLICANT:  BERGSMA, DERK J.
;    APPLICANT:  ELLIS, CATHERINE E.
;    TITLE OF INVENTION:  NOVEL G-PROTEIN COUPLED
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/846,704
;      FILING DATE:  30-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PRESTIA, PAUL F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  GH-70002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1564 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-846-704-1

  Query Match             99.7%;  Score 1274.8;  DB 3;  Length 1564;
  Best Local Similarity   99.8%;  Pred. No. 3.2e-287;
  Matches 1276;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053
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Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
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Db       1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
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Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
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Db       1354 TCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy       1261 ACCACAGTGCTGCCCTGA 1278
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Db       1414 ACCACAGTGCTGCCCTGA 1431
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RESULT 3
US-08-846-704-3
; Sequence 3, Application US/08846704
; Patent No. 6020157
;  GENERAL INFORMATION:
;    APPLICANT:  BERGSMA, DERK J.
;    APPLICANT:  ELLIS, CATHERINE E.
;    TITLE OF INVENTION:  NOVEL G-PROTEIN COUPLED
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/846,704
;      FILING DATE:  30-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
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;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  PRESTIA, PAUL F
;       REGISTRATION NUMBER:  23,031
;       REFERENCE/DOCKET NUMBER:  GH-70002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  610-407-0700
;       TELEFAX:  610-407-0701
;       TELEX:  846169
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1564 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-846-704-3

  Query Match             99.7%;  Score 1274.8;  DB 3;  Length 1564;
  Best Local Similarity   99.8%;  Pred. No. 3.2e-287;
  Matches 1276;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693
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Qy       541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db       694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy       601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db       754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db       814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db       874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
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Db       934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db      1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy      1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
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Db      1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy      1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
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Db      1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy      1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
            |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1354 TCCTTGTAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy      1261 ACCACAGTGCTGCCCTGA 1278
            ||||||||||||||||||
Db      1414 ACCACAGTGCTGCCCTGA 1431
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RESULT 4
US-08-462-509B-1
; Sequence 1, Application US/08462509B

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; Patent No. 6410701
;  GENERAL INFORMATION:
;    APPLICANT:  Soppet, Daniel et al
;    TITLE OF INVENTION:  Human Neuropeptide Receptor
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockiville
;      STATE:  MD
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,509B
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US95/05616
;      FILING DATE:  05-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wales, Michele M.
;      REGISTRATION NUMBER:  43,975
;      REFERENCE/DOCKET NUMBER:  PF168P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-309-8504
;      TELEFAX:  301-309-8439
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1209 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1209
US-08-462-509B-1

  Query Match             94.4%;  Score 1205.8;  DB 4;  Length 1209;
  Best Local Similarity   99.8%;  Pred. No. 3.2e-271;
  Matches 1207;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200

Qy       1201 TCCTTGCAG 1209
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Db       1201 TCCTTGTAG 1209
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RESULT 5
PCT-US95-05616-1
; Sequence 1, Application PC/TUS9505616
;  GENERAL INFORMATION:
;    APPLICANT:  LI, ET AL.
;    TITLE OF INVENTION:  Human Neuropeptide Receptor
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05616
;      FILING DATE:  concurrently
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-268
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1209 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  cDNA
PCT-US95-05616-1
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Query Match 94.0%; Score 1201; DB 5; Length 1209;
Best Local Similarity 99.6%; Pred. No. 4.2e-270;
Matches 1204; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCCCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
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Db       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
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Db       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200

Qy       1201 TCCTTGCAG 1209
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Db       1201 TCCTTGTAG 1209
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RESULT 6
US-08-846-705-3
; Sequence 3, Application US/08846705
; Patent No. 5935814
; GENERAL INFORMATION:
; APPLICANT: BERGSMA, DERK J.
; APPLICANT: ELLIS, CATHERINE E
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,705
; FILING DATE: 30-APR-1997

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;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  PRESTIA, PAUL F
;       REGISTRATION NUMBER:  23,031
;       REFERENCE/DOCKET NUMBER:  GH-70003
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  610-407-0700
;       TELEFAX:  610-407-0701
;       TELEX:  846169
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1133 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-846-705-3

  Query Match             85.0%;  Score 1086.4;  DB 2;  Length 1133;
  Best Local Similarity   99.9%;  Pred. No. 1.8e-243;
  Matches 1087;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
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Db       1081 CTCAGTGG 1088
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RESULT 7
US-08-846-705-1
; Sequence 1, Application US/08846705
; Patent No. 5935814
; GENERAL INFORMATION:
; APPLICANT: BERGSMA, DERK J.
; APPLICANT: ELLIS, CATHERINE E
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980

; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,705
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-846-705-1

Query Match 85.0%; Score 1086.4; DB 2; Length 1170;
Best Local Similarity 99.9%; Pred. No. 1.8e-243;
Matches 1087; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
              ||||||||
Db       1081 CTCAGTGG 1088
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RESULT 8
US-08-462-509B-3
; Sequence 3, Application US/08462509B
; Patent No. 6410701
;  GENERAL INFORMATION:
;    APPLICANT:  Soppet, Daniel et al
;    TITLE OF INVENTION:  Human Neuropeptide Receptor
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockiville
;      STATE:  MD
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,509B
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US95/05616
;      FILING DATE:  05-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wales, Michele M.
;      REGISTRATION NUMBER:  43,975
;      REFERENCE/DOCKET NUMBER:  PF168P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-309-8504
;      TELEFAX:  301-309-8439
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1110 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1110
US-08-462-509B-3

  Query Match             85.0%;  Score 1085.8;  DB 4;  Length 1110;
  Best Local Similarity   99.8%;  Pred. No. 2.4e-243;
  Matches 1087;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGC 1089
              |||||||||
Db       1081 CTCAGTGGC 1089


RESULT 9
US-08-462-509B-5
; Sequence 5, Application US/08462509B
; Patent No. 6410701
;  GENERAL INFORMATION:
;    APPLICANT:  Soppet, Daniel et al
;    TITLE OF INVENTION:  Human Neuropeptide Receptor
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockiville
;      STATE:  MD
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,509B
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US95/05616
;      FILING DATE:  05-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wales, Michele M.
;      REGISTRATION NUMBER:  43,975
;      REFERENCE/DOCKET NUMBER:  PF168P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  301-309-8504
;      TELEFAX:  301-309-8439
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1116 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1116
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US-08-462-509B-5

Query Match 84.8%; Score 1083.2; DB 4; Length 1116;
Best Local Similarity 99.7%; Pred. No. 9.7e-243;
Matches 1085; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGACCCC 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
```

```
Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
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Db       1081 CTCAGTGG 1088
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RESULT 10
PCT-US95-05616-5
; Sequence 5, Application PC/TUS9505616
;  GENERAL INFORMATION:
;    APPLICANT:  LI, ET AL.
;    TITLE OF INVENTION:  Human Neuropeptide Receptor
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05616
;      FILING DATE:  concurrently
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-268
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
```

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1133 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
PCT-US95-05616-5

Query Match 84.8%; Score 1083.2; DB 5; Length 1133;
Best Local Similarity 99.7%; Pred. No. 9.8e-243;
Matches 1085; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGACCCC 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
              ||||||||
Db       1081 CTCAGTGG 1088
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RESULT 11
PCT-US95-05616-3
; Sequence 3, Application PC/TUS9505616
;  GENERAL INFORMATION:
;    APPLICANT:  LI, ET AL.
;    TITLE OF INVENTION:  Human Neuropeptide Receptor
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05616
;      FILING DATE:  concurrently
;      CLASSIFICATION:
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-268
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1110 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  cDNA
PCT-US95-05616-3

  Query Match             84.3%;  Score 1077.8;  DB 5;  Length 1110;
  Best Local Similarity   99.4%;  Pred. No. 1.7e-241;
  Matches 1082;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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                ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
                ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
                |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGC 1089
                |||||||||
Db       1081 CTCAGTGGC 1089
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RESULT 12
US-08-513-974B-375
; Sequence 375, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street

```
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/513,974B
;       FILING DATE:  14-SEP-1995
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/JP95/01599
;       FILING DATE:  10-AUG-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-093989
;       FILING DATE:  19-AUG-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-057186
;       FILING DATE:  16-MAR-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-007177
;       FILING DATE:  20-JAN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-326611
;       FILING DATE:  28-DEC-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-270017
;       FILING DATE:  02-NOV-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-236357
;       FILING DATE:  30-SEP-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-236356
;       FILING DATE:  30-SEP-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189274
;       FILING DATE:  11-AUG-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189273
;       FILING DATE:  11-AUG-1945
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189272
;       FILING DATE:  11-AUG-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Resnick, David S.
;       REGISTRATION NUMBER:  34,235
;       REFERENCE/DOCKET NUMBER:  45753
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-523-3400
;       TELEFAX:  617-523-6440
;   INFORMATION FOR SEQ ID NO:  375:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  843 base pairs
;       TYPE:  nucleic acid
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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 28..816
US-08-513-974B-375

Query Match 54.7%; Score 699.2; DB 3; Length 843;
Best Local Similarity 90.0%; Pred. No. 1.6e-153;
Matches 749; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

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Qy        252 CATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCT 311
              | |  ||| |||||| ||||| || || |||||||| || ||||||||||||||||| ||
Db          9 CGTGTTCATCCTGTCACTGGCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCT 68

Qy        312 GCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTA 371
              |||||| |||||||| || |||||||| || ||||||||||||||||||||||||||||
Db         69 GCTGGTAGACATCACGGAATCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTA 128

Qy        372 TCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCG 431
              ||||||||| ||||||||||||||||  ||||| |||||||||| ||||||||||||||
Db        129 TCTACAGGCCGTGTCCGTGTCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCG 188

Qy        432 CTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTC 491
              |||||| |||||||||||||| || |||||||||||| |||||||| ||||| |||||
Db        189 CTGGTACGCCATCTGCCACCCGCTGTTGTTCAAGAGCACTGCCCGGCGCGCCCGCGGCTC 248

Qy        492 CATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGA 551
              |||||| |||||||||| |||||||||| |||||||||| |||||||| ||||||||
Db        249 CATCCTCGGCATCTGGGCGGTGTCGCTGGCTGTCATGGTGCCTCAGGCTGCTGTCATGGA 308

Qy        552 ATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGA 611
              || ||||| |||||||| ||||| |||||||||| || ||| | || ||||||||||
Db        309 GTGTAGCAGCGTGCTGCCCGAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGA 368

Qy        612 ACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTA 671
              |||||||||| ||||| || |||||||||||||||| |||||||| ||||||||||
Db        369 GCGCTGGGCAGACGACCTGTACCCCAAGATCTACCACAGCTGCTTCTTCATTGTCACCTA 428

Qy        672 CCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGG 731
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        429 CCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGG 488

Qy        732 CCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCA 791
              |||||||||||||||||||||| ||||||||| |||||||||| ||||||||||
Db        489 CCGCCAGATCCCCGGCACCACCTCGGCCCTGGTGCGCAACTGGAAGCGGCCCTCAGACCA 548

Qy        792 GCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCT 851
              |||||  |||| ||  |||||||||||  ||||||||||||||||||||||||||||||
Db        549 GCTGGACGACCAGGGCCAGGGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCGCGCCTTCCT 608

Qy        852 GGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCT 911
              ||| || ||||| |||||||| || |||||||||| ||||||||||||||||||||||
Db        609 GGCCGAGGTGAAACAGATGCGAGCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGCT 668

Qy        912 GCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTT 971
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                ||||||||||||||||||||||||||||||||| |||||||| ||||| |||||||| ||
Db        669 GCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGTGTCCTCAACGTCCTCAAGAGGGTCTT 728

Qy        972 CGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCA 1031
                ||||||||||||||||||||| ||||| || ||  |||||||||||||||||||||||||
Db        729 CGGGATGTTCCGCCAAGCCAGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCA 788

Qy       1032 CTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTC 1083
                ||||||||||||||||||||||| ||||| ||| || |||||  |||||||
Db        789 CTGGCTGGTGTACGCCAACAGCGCCGCCAATCCCCTCCTCTACTCCTTCCTC 840


RESULT 13
US-08-513-974B-55
; Sequence 55, Application US/08513974B
; Patent No. 6114139
;  GENERAL INFORMATION:
;    APPLICANT:  Hinuma, Shuji
;    APPLICANT:  Hosoya, Masaki
;    APPLICANT:  Fujii, Ryo
;    APPLICANT:  Ohtaki, Tetsuya
;    APPLICANT:  Fukusumi, Shoji
;    APPLICANT:  Ohgi, Kazuhiro
;    TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTOR PROTEIN,
;    TITLE OF INVENTION:  PRODUCTION, AND USE THEREOF
;    NUMBER OF SEQUENCES:  380
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/513,974B
;      FILING DATE:  14-SEP-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP95/01599
;      FILING DATE:  10-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-093989
;      FILING DATE:  19-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-057186
;      FILING DATE:  16-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-007177
;      FILING DATE:  20-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-326611
;      FILING DATE:  28-DEC-1994
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1945
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-513-974B-55

Query Match 52.6%; Score 672.2; DB 3; Length 789;
Best Local Similarity 90.7%; Pred. No. 2.9e-147;
Matches 716; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

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Qy        271 GCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAG 330
              || || || |||||||| || |||||||||||||||| |||||||| |||||||| ||
Db          1 GCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCTGCTGGTAGACATCACGGAA 60

Qy        331 TCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTG 390
              |||||||| || |||||||||||||||||||||||||||||||||||| |||||||||
Db         61 TCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCCGTGTCCGTG 120

Qy        391 TCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATGCCATCTGCCAC 450
              |||||||  ||||| |||||||||| |||||||||||||||||||| ||||||||||||
Db        121 TCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCGCTGGTACGCCATCTGCCAC 180

Qy        451 CCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCT 510
              || || ||||||||||||| |||||||| ||||| |||||||||| ||||||||||
Db        181 CCGCTGTTGTTCAAGAGCACTGCCCGGCGCGCCCGCGGCTCCATCCTCGGCATCTGGGCG 240

Qy        511 GTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCT 570
              |||||||||||  |||||||||| |||||||| |||||||| || ||||| ||||||||
Db        241 GTGTCGCTGGCTGTCATGGTGCCTCAGGCTGCTGTCATGGAGTGTAGCAGCGTGCTGCCC 300
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Qy        571 GAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTC 630
              ||||| |||||||||||| || ||| | || |||||||||||| |||||||||||| |||||
Db        301 GAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGAGCGCTGGGCAGACGACCTG 360

Qy        631 TATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTC 690
              || |||||||||||||||| |||||||| ||||||||||||||||||||||||||||||
Db        361 TACCCCAAGATCTACCACAGCTGCTTCTTCATTGTCACCTACCTGGCCCCACTGGGCCTC 420

Qy        691 ATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 750
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        421 ATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 480

Qy        751 ACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAG 810
              ||||| || |||||||| |||||||||| |||||||||||||||  |||| ||  |||
Db        481 ACCTCGGCCCTGGTGCGCAACTGGAAGCGGCCCTCAGACCAGCTGGACGACCAGGGCCAG 540

Qy        811 GGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATG 870
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Db        541 GGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCCGAGGTGAAACAGATG 600

Qy        871 CGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC 930
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Db        601 CGAGCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC 660

Qy        931 TACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCC 990
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Db        661 TACCTGCCCATCAGTGTCCTCAACGTCCTCAAGAGGGTCTTCGGGATGTTCCGCCAAGCC 720

Qy        991 AGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 1050
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Qy       1051 AGCGCTGCC 1059
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Db        781 AGCGCCGCC 789
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RESULT 14
US-09-461-436B-55
; Sequence 55, Application US/09461436B
; Patent No. 6538107
;   GENERAL INFORMATION:
;        APPLICANT: Shuji Hinuma
;                   Yasuaki Ito
;                   Ryo Fujii
;        TITLE OF INVENTION: G Protein Coupled Receptor Protein,
;                            Production, And Use Thereof
;        NUMBER OF SEQUENCES: 61
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Edwards & Angell, LLP
;             STREET: 101 Federal Street
;             CITY: BOSTON
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02209
;        COMPUTER READABLE FORM:
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;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/461,436B
;              FILING DATE: 14-Dec-1999
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 08/513,974
;              FILING DATE: 14-SEP-1995
;              APPLICATION NUMBER: PCT/JP95/01599
;              FILING DATE: 10-AUG-1995
;              APPLICATION NUMBER: 7-093989
;              FILING DATE: 19-APR-1995
;              APPLICATION NUMBER: 7-057186
;              FILING DATE: 16-MAR-1995
;              APPLICATION NUMBER: 7-007177
;              FILING DATE: 20-JAN-1995
;              APPLICATION NUMBER: 6-326611
;              FILING DATE: 28-DEC-1994
;              APPLICATION NUMBER: 6-270017
;              FILING DATE: 02-NOV-1994
;              APPLICATION NUMBER: 6-236357
;              FILING DATE: 30-SEP-1994
;              APPLICATION NUMBER: 6-236356
;              FILING DATE: 30-SEP-1994
;              APPLICATION NUMBER: 6-189274
;              FILING DATE: 11-AUG-1994
;              APPLICATION NUMBER: 6-189273
;              FILING DATE: 11-AUG-1994
;              APPLICATION NUMBER: 6-189272
;              FILING DATE: 11-AUG-1994
;         ATTORNEY/AGENT INFORMATION:
;              NAME: CONLIN, DAVID G.
;              REGISTRATION NUMBER: <Unknown>
;              REFERENCE/DOCKET NUMBER: 45753 DIV2
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 617-439-4444
;              TELEFAX: 617-439-4170
;    INFORMATION FOR SEQ ID NO: 55:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 789 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: double
;              TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-461-436B-55

  Query Match             52.6%;  Score 672.2;  DB 4;  Length 789;
  Best Local Similarity   90.7%;  Pred. No. 2.9e-147;
  Matches  716;  Conservative    0;  Mismatches   73;  Indels    0;  Gaps    0;

Qy        271 GCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAG 330
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Qy        331 TCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTG 390
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Db         61 TCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCCGTGTCCGTG 120

Qy        391 TCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATGCCATCTGCCAC 450
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Qy        451 CCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCT 510
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Qy        511 GTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCT 570
              |||||||||||  |||||||||| |||||||| |||||||| || ||||| ||||||||
Db        241 GTGTCGCTGGCTGTCATGGTGCCTCAGGCTGCTGTCATGGAGTGTAGCAGCGTGCTGCCC 300

Qy        571 GAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTC 630
              ||||| |||||||||||| || ||| | || |||||||||||| |||||||||||  |||||
Db        301 GAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGAGCGCTGGGCAGACGACCTG 360

Qy        631 TATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTC 690
              || |||||||||||||||| |||||||| ||||||||||||||||||||||||||||||
Db        361 TACCCCAAGATCTACCACAGCTGCTTCTTCATTGTCACCTACCTGGCCCCACTGGGCCTC 420

Qy        691 ATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 750
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        421 ATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 480

Qy        751 ACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAG 810
              ||||| || |||||||| |||||||||| ||||||||||||||  |||| ||  |||
Db        481 ACCTCGGCCCTGGTGCGCAACTGGAAGCGGCCCTCAGACCAGCTGGACGACCAGGGCCAG 540

Qy        811 GGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATG 870
              ||||||||   |||||||||||||||||||||||||||||| || ||||| ||||||
Db        541 GGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCCGAGGTGAAACAGATG 600

Qy        871 CGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC 930
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Qy        931 TACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCC 990
              |||||||||||||| |||||||| ||||| |||||||| ||||||||||||||||||||
Db        661 TACCTGCCCATCAGTGTCCTCAACGTCCTCAAGAGGGTCTTCGGGATGTTCCGCCAAGCC 720

Qy        991 AGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 1050
              || ||||| || ||  ||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 780

Qy       1051 AGCGCTGCC 1059
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Db        781 AGCGCCGCC 789
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RESULT 15
US-09-119-788-1
; Sequence 1, Application US/09119788

; Patent No. 6166193
; GENERAL INFORMATION:
; APPLICANT: Yanagisawa, Masashi
; TITLE OF INVENTION: CDNA CLONE MY1 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/119,788
; FILING DATE: 21-JUL-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,790
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: GH50029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5515
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1633 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-09-119-788-1

Query Match 43.4%; Score 554.4; DB 3; Length 1633;
Best Local Similarity 68.2%; Pred. No. 8.3e-120;
Matches 819; Conservative 0; Mismatches 366; Indels 15; Gaps 3;

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Qy         80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
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Qy        140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
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Qy        200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
              | ||  |||| ||||||  |||||||||||||||||| || |||||||||||||| ||||
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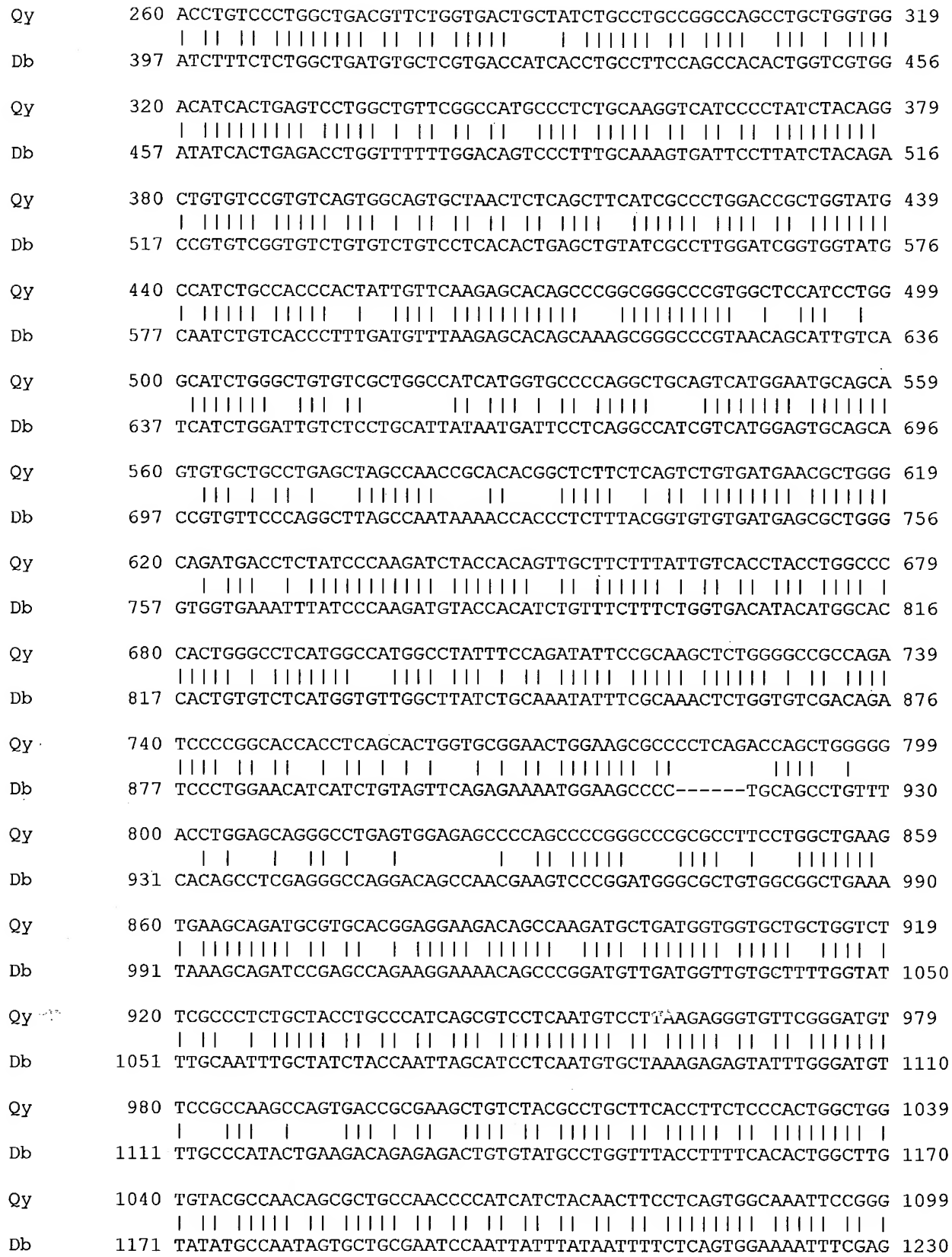

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Db       1231 AGGAATTTAAAGCTGCGTTTTCTTGCTGTTGCCTTGGAGTTCACCATCGCCAGGAGGATC 1290

Qy       1157 TGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTGTCCTTGCAGAGCCGAT 1216
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Job time : 103.178 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 19:59:43 ; Search time 659.145 Seconds
(without alignments)
9829.265 Million cell updates/sec

Title: US-10-070-532-1
Perfect score: 1278
Sequence: 1 atggagccctcagccacccc.....tcaccacagtgctgccctga 1278

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query

	No.	Score	Match	Length	DB	ID	Description
	1	1274.8	99.7	1564	9	US-09-828-538-23	Sequence 23, Appl
	2	1274.8	99.7	1564	15	US-10-225-567A-367	Sequence 367, App
	3	1274.8	99.7	1564	16	US-10-352-684A-21	Sequence 21, Appl
	4	1270	99.4	1278	11	US-09-826-509-548	Sequence 548, App
	5	1207.4	94.5	1209	14	US-10-077-874-1	Sequence 1, Appli
	6	1201	94.0	1209	10	US-09-393-696-1	Sequence 1, Appli
	7	1085.8	85.0	1110	14	US-10-077-874-3	Sequence 3, Appli
	8	1083.2	84.8	1116	14	US-10-077-874-5	Sequence 5, Appli
	9	1083.2	84.8	1133	10	US-09-393-696-5	Sequence 5, Appli
	10	1083	84.7	1281	9	US-09-730-931-1	Sequence 1, Appli
	11	1077.8	84.3	1110	10	US-09-393-696-3	Sequence 3, Appli
	12	672.2	52.6	789	15	US-10-278-087A-55	Sequence 55, Appl
	13	554.4	43.4	1633	15	US-10-282-717-1	Sequence 1, Appli
	14	554.4	43.4	1843	15	US-10-225-567A-369	Sequence 369, App
	15	549.6	43.0	1335	11	US-09-826-509-550	Sequence 550, App
	16	249.2	19.5	9785	9	US-09-961-848-1	Sequence 1, Appli
	17	249.2	19.5	10453	9	US-09-828-538-21	Sequence 21, Appl
	18	244	19.1	244	9	US-09-828-538-6	Sequence 6, Appli
	19	227	17.8	227	9	US-09-828-538-10	Sequence 10, Appl
	20	199	15.6	356	9	US-09-828-538-2	Sequence 2, Appli
	21	189.4	14.8	324	9	US-09-828-538-14	Sequence 14, Appl
	22	179	14.0	179	9	US-09-828-538-4	Sequence 4, Appli
	23	163.2	12.8	1290	17	US-10-719-587-55	Sequence 55, Appl
	24	163.2	12.8	1290	17	US-10-719-587-56	Sequence 56, Appl
	25	163.2	12.8	1293	9	US-09-866-248A-7	Sequence 7, Appli
	26	163.2	12.8	1293	15	US-10-225-567A-657	Sequence 657, App
	27	163.2	12.8	1320	9	US-09-292-973-3	Sequence 3, Appli
	28	156.2	12.2	1299	17	US-10-719-587-38	Sequence 38, Appl
	29	156.2	12.2	1410	9	US-09-866-248A-1	Sequence 1, Appli
	30	149.8	11.7	1532	9	US-09-292-973-1	Sequence 1, Appli
	31	128.4	10.0	168575	15	US-10-178-194-1	Sequence 1, Appli
	32	126	9.9	977	12	US-09-876-143-1561	Sequence 1561, Ap
	33	122	9.5	122	9	US-09-828-538-12	Sequence 12, Appl
	34	120.6	9.4	1174	17	US-10-611-210-9	Sequence 9, Appli
	35	119	9.3	1110	14	US-10-044-592-17	Sequence 17, Appl
	36	119	9.3	1110	15	US-10-278-087A-31	Sequence 31, Appl
	37	119	9.3	1113	15	US-10-225-567A-244	Sequence 244, App
	38	119	9.3	1152	17	US-10-611-210-10	Sequence 10, Appl
	39	119	9.3	1174	17	US-10-611-210-7	Sequence 7, Appli
	40	119	9.3	1331	14	US-10-044-592-73	Sequence 73, Appl
	41	118.4	9.3	1173	17	US-10-611-210-6	Sequence 6, Appli
	42	116	9.1	116	9	US-09-828-538-8	Sequence 8, Appli
	43	115.8	9.1	1174	17	US-10-611-210-8	Sequence 8, Appli
	44	107.2	8.4	669	14	US-10-044-592-70	Sequence 70, Appl
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ALIGNMENTS

RESULT 1
US-09-828-538-23
; Sequence 23, Application US/09828538
; Patent No. US20010025031A1
; GENERAL INFORMATION:

; APPLICANT: Ellis, Catherine E.
; APPLICANT: Kwok, Cheni
; APPLICANT: Bodsworth, Nicola J.
; APPLICANT: Halsey, Wendy
; APPLICANT: Van Horn, Stephanie
; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods
; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications
; FILE REFERENCE: GH-50038-C1
; CURRENT APPLICATION NUMBER: US/09/828,538
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/088,624
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: 60/093,726
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: 09/328,014
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 1564
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-828-538-23

Query Match 99.7%; Score 1274.8; DB 9; Length 1564;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Qy      841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Db      994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy      901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Db     1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy      961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Db     1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy     1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Db     1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy     1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140

Db     1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy     1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200

Db     1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy     1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260

Db     1354 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy     1261 ACCACAGTGCTGCCCTGA 1278
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Db        1414 ACCACAGTGCTGCCCTGA 1431


RESULT 2
US-10-225-567A-367
; Sequence 367, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
;  APPLICANT: LifeSpan Biosciences
;  APPLICANT:  Brown, Joseph P.
;  APPLICANT:  Burmer, Glenna C.
;  APPLICANT:  Roush, Christine L.
;  TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
;  FILE REFERENCE: 1920-4-4
;  CURRENT APPLICATION NUMBER: US/10/225,567A
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/257,144
;  PRIOR FILING DATE: 2000-12-19
;  NUMBER OF SEQ ID NOS: 2292
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 367
;   LENGTH: 1564
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-225-567A-367

  Query Match             99.7%;  Score 1274.8;  DB 15;  Length 1564;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1276;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        934 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1354 TCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413
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Qy       1261 ACCACAGTGCTGCCCTGA 1278
              ||||||||||||||||||
Db       1414 ACCACAGTGCTGCCCTGA 1431


RESULT 3
US-10-352-684A-21
; Sequence 21, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals Inc.
;  APPLICANT:  Carroll, Joseph M.
;  APPLICANT:  Healy, Aileen
;  APPLICANT:  Weich, Nadine S.
;  APPLICANT:  Kelly, Louise M.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
;  TITLE OF INVENTION:  HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303,
13906,
;  TITLE OF INVENTION:  15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
;  TITLE OF INVENTION:  1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847,
1849,
;  TITLE OF INVENTION:  15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
;  FILE REFERENCE: MPI02-019P1RNOMNIM
;  CURRENT APPLICATION NUMBER: US/10/352,684A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: US 60/354,333
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: US 60/360,258
;  PRIOR FILING DATE: 2002-02-28
;  PRIOR APPLICATION NUMBER: US 60/364,476
;  PRIOR FILING DATE: 2002-03-15
;  PRIOR APPLICATION NUMBER: US 60/375,626
;  PRIOR FILING DATE: 2002-04-26
;  PRIOR APPLICATION NUMBER: US 60/386,494
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US 60/390,965
;  PRIOR FILING DATE: 2002-06-24
;  PRIOR APPLICATION NUMBER: US 60/392,480
;  PRIOR FILING DATE: 2002-06-28
;  PRIOR APPLICATION NUMBER: US 60/394,128
;  PRIOR FILING DATE: 2002-07-03
;  PRIOR APPLICATION NUMBER: US 60/399,783
;  PRIOR FILING DATE: 2002-07-31
;  PRIOR APPLICATION NUMBER: US 60/403,221
;  PRIOR FILING DATE: 2002-08-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 62
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 1564
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)...(1431)
US-10-352-684A-21
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Query Match 99.7%; Score 1274.8; DB 16; Length 1564;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1276; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933
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Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1293

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
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Db       1294 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1353

Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1354 TCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1413

Qy       1261 ACCACAGTGCTGCCCTGA 1278
              ||||||||||||||||||
Db       1414 ACCACAGTGCTGCCCTGA 1431
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RESULT 4
US-09-826-509-548
; Sequence 548, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1

; SEQ ID NO 548
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-548

Query Match 99.4%; Score 1270; DB 11; Length 1278;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1273; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAAAAAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200

Qy       1201 TCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1201 TCCTTGCAGAGCCGATGCTCCATCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTC 1260

Qy       1261 ACCACAGTGCTGCCCTGA 1278
              ||||||||||||||||||
Db       1261 ACCACAGTGCTGCCCTGA 1278
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RESULT 5
US-10-077-874-1
; Sequence 1, Application US/10077874
; Publication No. US20020115155A1
;   GENERAL INFORMATION:
;        APPLICANT: Soppet, Daniel et al
;        TITLE OF INVENTION: Human Neuropeptide Receptor
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: MD
;             COUNTRY: USA
;             ZIP: 20850
```

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;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/077,874
;              FILING DATE: 20-Feb-2002
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 08/462,509
;              FILING DATE: 05-JUNE-1995
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Wales, Michele M.
;              REGISTRATION NUMBER: 43,975
;              REFERENCE/DOCKET NUMBER: PF168P1D1
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 301-309-8504
;              TELEFAX: 301-309-8439
;    INFORMATION FOR SEQ ID NO: 1:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 1209 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         FEATURE:
;              NAME/KEY:  CDS
;              LOCATION:  1..1209
;         SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-077-874-1

  Query Match             94.5%;  Score 1207.4;  DB 14;  Length 1209;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1208;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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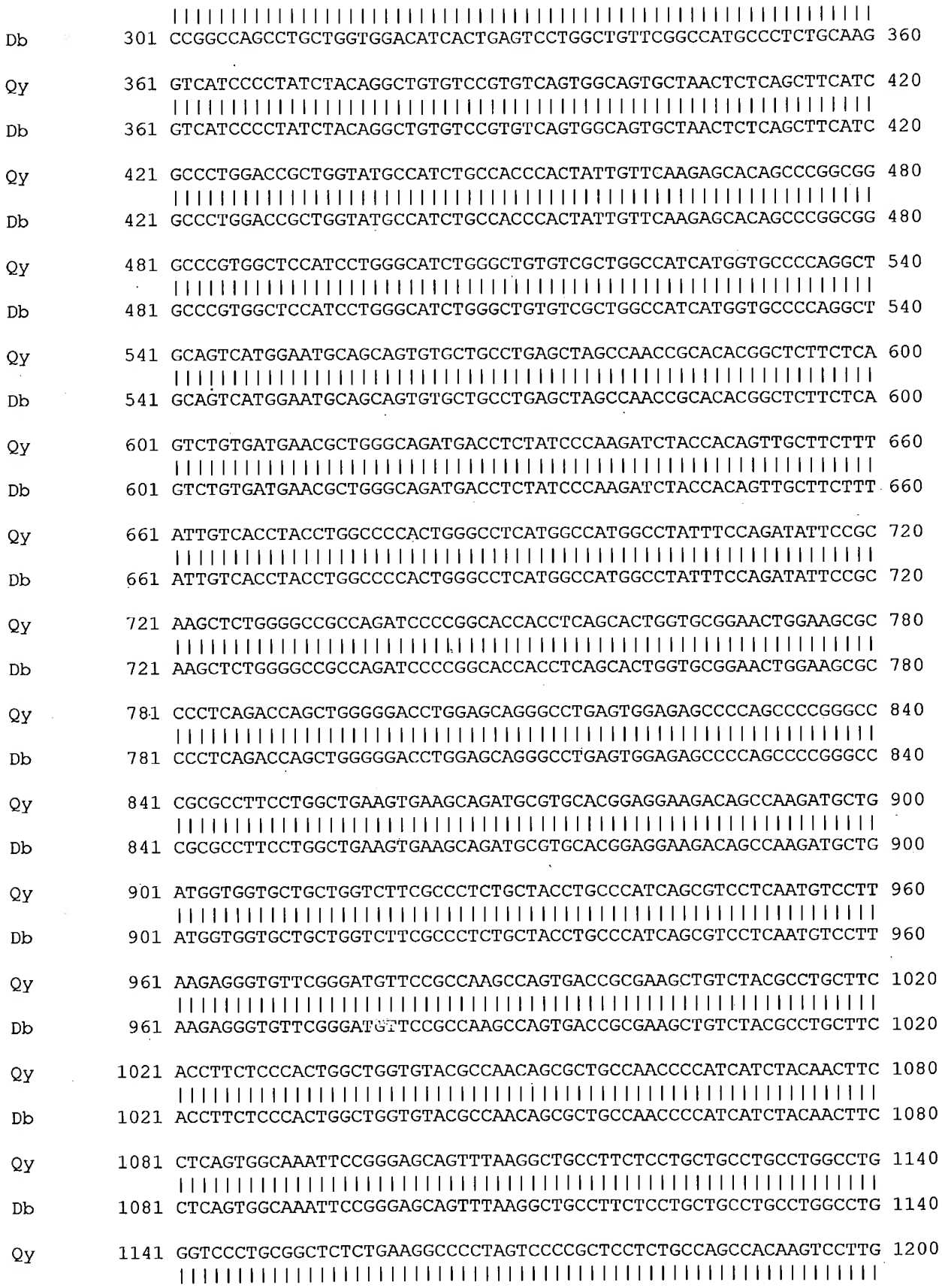

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Db       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200

Qy       1201 TCCTTGCAG 1209
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Db       1201 TCCTTGTAG 1209


RESULT 6
US-09-393-696-1
; Sequence 1, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc. et al.
;  TITLE OF INVENTION: Human Neuropeptide Receptor
;  FILE REFERENCE: PF168P2
;  CURRENT APPLICATION NUMBER: US/09/393,696
;  CURRENT FILING DATE: 1999-09-10
;  EARLIER APPLICATION NUMBER: PCT/US95/05616
;  EARLIER FILING DATE: 1995-05-05
;  EARLIER APPLICATION NUMBER: US08/462,509
;  EARLIER FILING DATE: 1995-06-05
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1209
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1209)
US-09-393-696-1

  Query Match             94.0%;  Score 1201;  DB 10;  Length 1209;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 1204;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCCCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCTGGCCTG 1140

Qy       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1141 GGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTG 1200

Qy       1201 TCCTTGCAG 1209
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Db       1201 TCCTTGTAG 1209


RESULT 7
US-10-077-874-3
; Sequence 3, Application US/10077874
; Publication No. US20020115155A1
;   GENERAL INFORMATION:
;        APPLICANT: Soppet, Daniel et al
;        TITLE OF INVENTION: Human Neuropeptide Receptor
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: MD
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/077,874
;             FILING DATE: 20-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/462,509
;             FILING DATE: 05-JUNE-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Wales, Michele M.
;             REGISTRATION NUMBER: 43,975
;             REFERENCE/DOCKET NUMBER: PF168P1D1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 301-309-8504
;             TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1110 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..1110
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-077-874-3

  Query Match             85.0%;  Score 1085.8;  DB 14;  Length 1110;
  Best Local Similarity   99.8%;  Pred. No. 6.6e-295;
  Matches 1087;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGC 1089
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Db       1081 CTCAGTGGC 1089
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RESULT 8
US-10-077-874-5
; Sequence 5, Application US/10077874
; Publication No. US20020115155A1
;   GENERAL INFORMATION:
;        APPLICANT: Soppet, Daniel et al
;        TITLE OF INVENTION: Human Neuropeptide Receptor
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: MD
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/077,874
;             FILING DATE: 20-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/462,509
;             FILING DATE: 05-JUNE-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Wales, Michele M.
;             REGISTRATION NUMBER: 43,975
;             REFERENCE/DOCKET NUMBER: PF168P1D1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 301-309-8504
;             TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
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;             LENGTH: 1116 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..1116
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-077-874-5

  Query Match             84.8%;  Score 1083.2;  DB 14;  Length 1116;
  Best Local Similarity   99.7%;  Pred. No. 3.6e-294;
  Matches 1085;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGACCCC 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
              ||||||||
Db       1081 CTCAGTGG 1088
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RESULT 9
US-09-393-696-5
; Sequence 5, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc. et al.
;  TITLE OF INVENTION: Human Neuropeptide Receptor
;  FILE REFERENCE: PF168P2
;  CURRENT APPLICATION NUMBER: US/09/393,696
;  CURRENT FILING DATE: 1999-09-10
;  EARLIER APPLICATION NUMBER: PCT/US95/05616
;  EARLIER FILING DATE: 1995-05-05
;  EARLIER APPLICATION NUMBER: US08/462,509
;  EARLIER FILING DATE: 1995-06-05
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1133
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
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; LOCATION: (1)..(1131)
US-09-393-696-5

Query Match 84.8%; Score 1083.2; DB 10; Length 1133;
Best Local Similarity 99.7%; Pred. No. 3.6e-294;
Matches 1085; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGACCCC 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
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Db       1081 CTCAGTGG 1088
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RESULT 10
US-09-730-931-1
; Sequence 1, Application US/09730931
; Patent No. US20020064814A1
; GENERAL INFORMATION:
;  APPLICANT:  ELLIS, CATHERINE E.
;  TITLE OF INVENTION:  DOG OREXIN 1 RECEPTOR
;  FILE REFERENCE:  GH-70669
;  CURRENT APPLICATION NUMBER: US/09/730,931
;  CURRENT FILING DATE:  2000-12-06
;  PRIOR APPLICATION NUMBER:  60/169,373
;  PRIOR FILING DATE:  1999-12-07
;  NUMBER OF SEQ ID NOS:  2
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 1281
;   TYPE: DNA
;   ORGANISM: CANIS FAMILIARIS
US-09-730-931-1

  Query Match             84.7%;  Score 1083;  DB 9;  Length 1281;
  Best Local Similarity   90.9%;  Pred. No. 4.2e-294;
  Matches 1165;  Conservative    0;  Mismatches  110;  Indels    6;  Gaps    1;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              |||||||||||||||||||||||||||||  |||  |||| | ||| || | |||| |
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGACTGGGACCCCCACCGGCGGCGGGGAGCTG 60

Qy         61 TCCCCT------GTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGAT 114
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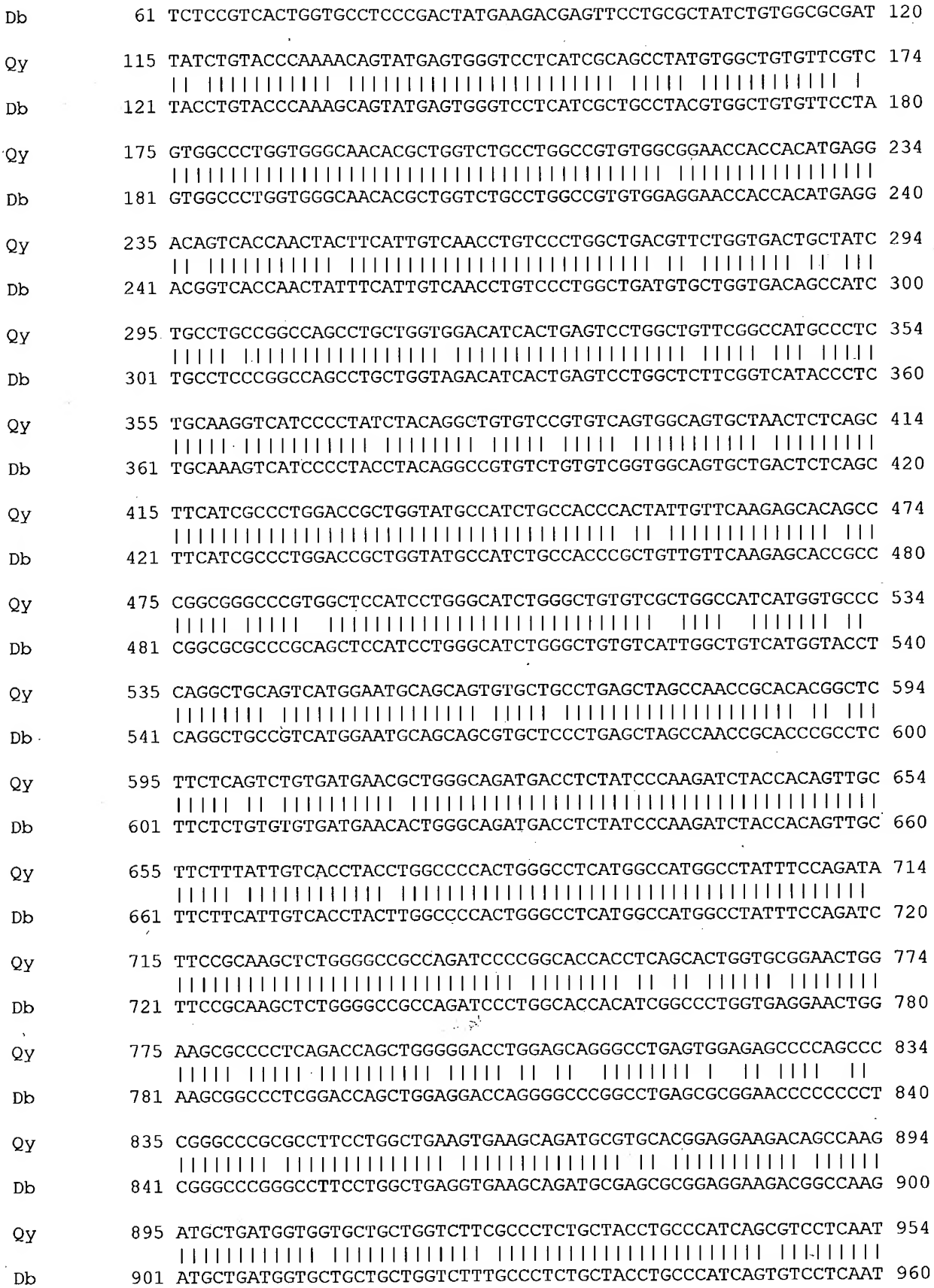

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Qy        955 GTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCC 1014
              ||||| ||||||||||||||||||||||||| |||||||||| ||||| || ||||||
Db        961 GTCCTCAAGAGGGTGTTCGGGATGTTCCGCCAATCCAGTGACCGAGAAGCCGTGTACGCC 1020

Qy       1015 TGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTAC 1074
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1021 TGCTTCACCTTCTCCCACTGGCTGGTGTATGCCAACAGCGCTGCCAACCCCATCATCTAC 1080

Qy       1075 AACTTCCTCAGTGGCAAATTCCGGGAGCAGTTTAAGGCTGCCTTCTCCTGCTGCCTGCCT 1134
              |||||||||| ||||||||||||||||||||||| ||||||||||||||||||||||
Db       1081 AACTTCCTCAGCGGCAAATTCCGGGAGCAGTTTAAGGCCGCCTTCTCCTGCTGCCTGCCT 1140

Qy       1135 GGCCTGGGTCCCTGCGGCTCTCTGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAG 1194
              |||||||||||||||||||| |||||||| || ||||||||||||||||||||||||
Db       1141 GGCCTGGGTCCCTGCGGCTCTCCGAAGGCCCCCAGCCCCCGCTCCTCTGCCAGCCACAAG 1200

Qy       1195 TCCTTGTCCTTGCAGAGCCGATGCTCCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACC 1254
              |||||||||||||| ||||| |||||||||||||| || | ||||| ||||||||||||
Db       1201 TCCTTGTCCTTGCACAGCCGGTGCTCCGTCTCCAAAGTCCCCGAGCACGTGGTGCTCACC 1260

Qy       1255 AGCGTCACCACAGTGCTGCCC 1275
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Db       1261 AGTGTCACCACGGTGCTGCCC 1281
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RESULT 11
US-09-393-696-3
; Sequence 3, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; FILE REFERENCE: PF168P2
; CURRENT APPLICATION NUMBER: US/09/393,696
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: PCT/US95/05616
; EARLIER FILING DATE: 1995-05-05
; EARLIER APPLICATION NUMBER: US08/462,509
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1110)
US-09-393-696-3

Query Match 84.3%; Score 1077.8; DB 10; Length 1110;
Best Local Similarity 99.4%; Pred. No. 1.2e-292;
Matches 1082; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
               ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960
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Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGC 1089
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Db       1081 CTCAGTGGC 1089
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RESULT 12
US-10-278-087A-55
; Sequence 55, Application US/10278087A
; Publication No. US20030138817A1
;   GENERAL INFORMATION:
;        APPLICANT: Shuji Hinuma
;                   Yasuaki Ito
;                   Ryo Fujii
;        TITLE OF INVENTION: G Protein Coupled Receptor Protein,
;                            Production, And Use Thereof
;        NUMBER OF SEQUENCES: 61
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Edwards & Angell, LLP
;             STREET: 101 Federal Street
;             CITY: BOSTON
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02209
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/278,087A
;             FILING DATE: 31-Jan-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/461,436
;             FILING DATE: 14-DEC-1999
;             APPLICATION NUMBER: 09/038,572
;             FILING DATE: 11-MAR-1998
;             APPLICATION NUMBER: 08/513,974
;             FILING DATE: 14-SEP-1995
;             APPLICATION NUMBER: PCT/JP95/01599
;             FILING DATE: 10-AUG-1995
;             APPLICATION NUMBER: 7-093989
;             FILING DATE: 19-APR-1995
;             APPLICATION NUMBER: 7-057186
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;              FILING DATE: 16-MAR-1995
;              APPLICATION NUMBER: 7-007177
;              FILING DATE: 20-JAN-1995
;              APPLICATION NUMBER: 6-326611
;              FILING DATE: 28-DEC-1994
;              APPLICATION NUMBER: 6-270017
;              FILING DATE: 02-NOV-1994
;              APPLICATION NUMBER: 6-236357
;              FILING DATE: 30-SEP-1994
;              APPLICATION NUMBER: 6-236356
;              FILING DATE: 30-SEP-1994
;              APPLICATION NUMBER: 6-189274
;              FILING DATE: 11-AUG-1994
;              APPLICATION NUMBER: 6-189273
;              FILING DATE: 11-AUG-1994
;              APPLICATION NUMBER: 6-189272
;              FILING DATE: 11-AUG-1994
;         ATTORNEY/AGENT INFORMATION:
;              NAME: CONLIN, DAVID G.
;              REGISTRATION NUMBER: <Unknown>
;              REFERENCE/DOCKET NUMBER: 45753 DIV3
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 617-439-4444
;              TELEFAX: 617-439-4170
;    INFORMATION FOR SEQ ID NO: 55:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 789 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: double
;              TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-10-278-087A-55

  Query Match             52.6%;  Score 672.2;  DB 15;  Length 789;
  Best Local Similarity   90.7%;  Pred. No. 1.1e-178;
  Matches  716;  Conservative    0;  Mismatches   73;  Indels    0;  Gaps    0;

Qy        271 GCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAG 330
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Db          1 GCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCTGCTGGTAGACATCACGGAA 60

Qy        331 TCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTG 390
              |||||||| || ||||||||||||||||||||||||||||||||||| |||||||||
Db         61 TCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCCGTGTCCGTG 120

Qy        391 TCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATGCCATCTGCCAC 450
              ||||||| ||||| |||||||||| |||||||||||||||||||| ||||||||||||
Db        121 TCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCGCTGGTACGCCATCTGCCAC 180

Qy        451 CCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCT 510
              || || |||||||||||||| |||||||| ||||| |||||||||| ||||||||||||
Db        181 CCGCTGTTGTTCAAGAGCACTGCCCGGCGCGCCCGCGGCTCCATCCTCGGCATCTGGGCG 240

Qy        511 GTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCT 570
              |||||||||||  |||||||||| |||||||| |||||||| || ||||| ||||||||
Db        241 GTGTCGCTGGCTGTCATGGTGCCTCAGGCTGCTGTCATGGAGTGTAGCAGCGTGCTGCCC 300
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Qy        571 GAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTC 630
              ||||| |||||||||||| || ||| | || |||||||||||| |||||||||||| |||||
Db        301 GAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGAGCGCTGGGCAGACGACCTG 360

Qy        631 TATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTC 690
              || |||||||||||||||||| |||||||| ||||||||||||||||||||||||||||||
Db        361 TACCCCAAGATCTACCACAGCTGCTTCTTCATTGTCACCTACCTGGCCCCACTGGGCCTC 420

Qy        691 ATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 750
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        421 ATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 480

Qy        751 ACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAG 810
              ||||| || |||||||| |||||||||| ||||||||||||||. |||| ||  |||
Db        481 ACCTCGGCCCTGGTGCGCAACTGGAAGCGGCCCTCAGACCAGCTGGACGACCAGGGCCAG 540

Qy        811 GGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATG 870
              ||||||||   |||||||||||||||||||||||||||||| || ||||| ||||||
Db        541 GGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCCGAGGTGAAACAGATG 600

Qy        871 CGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC 930
              || || |||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        601 CGAGCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC 660

Qy        931 TACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCC 990
              |||||||||||||| |||||||| ||||| |||||||| ||||||||||||||||||||
Db        661 TACCTGCCCATCAGTGTCCTCAACGTCCTCAAGAGGGTCTTCGGGATGTTCCGCCAAGCC 720

Qy        991 AGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 1050
              || ||||| || ||  ||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 780

Qy       1051 AGCGCTGCC 1059
              ||||| |||
Db        781 AGCGCCGCC 789
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RESULT 13
US-10-282-717-1
; Sequence 1, Application US/10282717
; Publication No. US20030083466A1
; GENERAL INFORMATION:
; APPLICANT: YANAGISAWA, MASASHI
; TITLE OF INVENTION: cDNA CLONE MY1 THAT ENCODES A NOVEL
; TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR
; FILE REFERENCE: GH50029D1C1
; CURRENT APPLICATION NUMBER: US/10/282,717
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/676,625
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/119,788
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: 60/053,790
; PRIOR FILING DATE: 1997-07-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1
; LENGTH: 1633
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-10-282-717-1

Query Match 43.4%; Score 554.4; DB 15; Length 1633;
Best Local Similarity 68.2%; Pred. No. 1.8e-145;
Matches 819; Conservative 0; Mismatches 366; Indels 15; Gaps 3;

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Qy        80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
             | || || || || || || || |||||| | || || ||| |||| ||| | |||||||
Db       217 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 276

Qy       140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
             ||||||| ||||| |  ||  |    |||||||||||||| ||  | || |||   ||||
Db       277 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 336

Qy       200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
             | ||  |||| |||||| |||||||||||||||||| || |||||||||||||| ||||
Db       337 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 396

Qy       260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
             | || || |||||||| || || |||||    | |||||| || ||||  ||| | ||||
Db       397 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 456

Qy       320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
             | ||||||||| ||||| | || || ||  |||| ||||| || || || |||||||||
Db       457 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 516

Qy       380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
             | ||||| ||||| ||| | || || || || |||| |||||| |||| || |||||||
Db       517 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 576

Qy       440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
             | ||||| |||||  |  |||| ||||||||||  ||||||||||  |  |||  |
Db       577 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 636

Qy       500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
              |||||||  ||| ||       || ||| | || |||||    |||||||| |||||||
Db       637 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 696

Qy       560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
              ||| | || |   |||||||    ||    |||||  | || ||||||||| |||||||
Db       697 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 756

Qy       620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
              | |||  | |||||||||||| |||||||  || |||||| | || || ||| |||| |
Db       757 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 816

Qy       680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
             |||||  | |||||||   |||| ||| | || ||||| ||||| |||||| | || ||||
Db       817 CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA 876

Qy       740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG 799
             |||| || ||  | || | | |   | | || |||||||  ||        ||||  |
Db       877 TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC------TGCAGCCTGTTT 930
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Qy        800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAG 859
              | |   |. || |   |         |  || |||||    ||||  |   |||||||
Db        931 CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGGGCGCTGTGGCGGCTGAAA 990

Qy        860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
              | |||||||| || ||  | ||||| ||||||  |||| |||||||  |||||  |||| |
Db        991 TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCCGGATGTTGATGGTTGTGCTTTTGGTAT 1050

Qy        920 TCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979
              | ||  | ||||| || || || ||| ||||||||||  || |||||  || || |||||||
Db       1051 TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 1110

Qy        980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039
              |   |||  |    ||| | ||  |||| || ||||| || ||||| || |||||||| |
Db       1111 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG 1170

Qy       1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGCAAATTCCGGG 1099
              | || ||||| || ||||| || || || || || || || |||||||| ||||| || |
Db       1171 TATATGCCAATAGTGCTGCGAATCCAATTATTTATAATTTTCTCAGTGGAAAATTTCGAG 1230

Qy       1100 AGCAGTTTAAGGCTGCCTTCTC---CTGCTGCCTGCCTGGCCTGGGTCCCTGCGGCTCTC 1156
              || | ||||| ||||| || ||   ||| |||||    |  |    || |   |    ||
Db       1231 AGGAATTTAAAGCTGCGTTTTCTTGCTGTTGCCTTGGAGTTCACCATCGCCAGGAGGATC 1290

Qy       1157 TGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTGTCCTTGCAGAGCCGAT 1216
              |    ||    | |       | | |  ||||  |||||||| ||   || | | |
Db       1291 GGCTCACCAGGGGACGAACTAGCACAGAGAGCCGGAAGTCCTTGACCACTCAAATCAGCA 1350

Qy       1217 GCT------CCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTCACCACAGTGC 1270
              ||      | | || ||| | |||||||| || |||||||| ||| | | |||| | |
Db       1351 ACTTTGATAACATATCAAAACTTTCTGAGCAAGTTGTGCTCACTAGCATAAGCACACTCC 1410
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RESULT 14
US-10-225-567A-369
; Sequence 369, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
;  APPLICANT: LifeSpan Biosciences
;  APPLICANT:  Brown, Joseph P.
;  APPLICANT:  Burmer, Glenna C.
;  APPLICANT:  Roush, Christine L.
;  TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
;  FILE REFERENCE: 1920-4-4
;  CURRENT APPLICATION NUMBER: US/10/225,567A
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/257,144
;  PRIOR FILING DATE: 2000-12-19
;  NUMBER OF SEQ ID NOS: 2292
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 369
;   LENGTH: 1843
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-225-567A-369
```

Query Match 43.4%; Score 554.4; DB 15; Length 1843;
Best Local Similarity 68.2%; Pred. No. 1.8e-145;
Matches 819; Conservative 0; Mismatches 366; Indels 15; Gaps 3;

```
Qy        80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
             | || || || || || || || |||||| | || || ||| |||| ||| | |||||||
Db       428 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 487

Qy       140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
             ||||||| ||||| |  ||  |    |||||||||||||| ||  | || |||   ||||
Db       488 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 547

Qy       200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
             | ||  |||| |||||| |||||||||||||||||| || |||||||||||||| ||||
Db       548 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 607

Qy       260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
             | || || |||||||| || || |||||    | |||||| || ||||  ||| | ||||
Db       608 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 667

Qy       320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
             | ||||||||| ||||| | || || ||  |||| ||||| || || || |||||||||
Db       668 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 727

Qy       380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
             | ||||| ||||| ||| | || || || || ||||  |||||| |||| || |||||||
Db       728 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 787

Qy       440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
             | ||||| |||||  |  |||| ||||||||||  |||||||||  |  |||  |
Db       788 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 847

Qy       500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
              |||||||  ||| ||       || ||| | || |||||    |||||||| |||||||
Db       848 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 907

Qy       560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
               ||| | || |   |||||||    ||    |||||  | || |||||||| |||||||
Db       908 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 967

Qy       620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
               | |||  | |||||||||||| |||||||  || |||||| | || || ||| |||| |
Db       968 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 1027

Qy       680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
             ||||| | |||||||   |||| ||| | || ||||| ||||| |||||| | || ||||
Db      1028 CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA 1087

Qy       740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG 799
             |||| || ||  | || | | |   | | || ||||||| ||        ||||  |
Db      1088 TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC------TGCAGCCTGTTT 1141

Qy       800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAG 859
               | |   | || |   |        |  || |||||    ||||  |   |||||||
Db      1142 CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGAGCGCTGTGGCGGCTGAAA 1201
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Qy        860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
              | |||||||| || ||  | ||||| |||||| |||| ||||||| |||||  |||| |
Db       1202 TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCCGGATGTTGATGGTTGTGCTTTTGGTAT 1261

Qy        920 TCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979
              | ||  | ||||| || || || ||| |||||||||| || ||||| || || |||||||
Db       1262 TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 1321

Qy        980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039
              |  ||| |   ||| | ||  |||| || ||||| || ||||| || |||||||| |
Db       1322 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG 1381

Qy       1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGCAAATTCCGGG 1099
              | || ||||| || ||||| || || || || || || || || |||||||| ||||| || |
Db       1382 TATATGCCAATAGTGCTGCGAATCCAATTATTTATAATTTTCTCAGTGGAAAATTTCGAG 1441

Qy       1100 AGCAGTTTAAGGCTGCCTTCTC---CTGCTGCCTGCCTGGCCTGGGTCCCTGCGGCTCTC 1156
              || | ||||| ||||| || ||   ||| |||||    |  |    || |   |    ||
Db       1442 AGGAATTTAAAGCTGCGTTTTCTTGCTGTTGCCTTGGAGTTCACCATCGCCAGGAGGATC 1501

Qy       1157 TGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTGTCCTTGCAGAGCCGAT 1216
               |    ||    | |       | | |  ||||  ||||||||| ||   || | | |
Db       1502 GGCTCACCAGGGGACGAACTAGCACAGAGAGCCGGAAGTCCTTGACCACTCAAATCAGCA 1561

Qy       1217 GCT------CCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTCACCACAGTGC 1270
               ||       | | || ||| | |||||||| || |||||||| ||| | | |||| | |
Db       1562 ACTTTGATAACATATCAAAACTTTCTGAGCAAGTTGTGCTCACTAGCATAAGCACACTCC 1621
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RESULT 15
US-09-826-509-550
; Sequence 550, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 550
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-550

Query Match 43.0%; Score 549.6; DB 11; Length 1335;
Best Local Similarity 68.0%; Pred. No. 3.7e-144;

Matches 816; Conservative 0; Mismatches 369; Indels 15; Gaps 3;

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Qy         80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
              |  ||  ||  ||  ||  ||  ||  ||  ||||||  |  ||  ||  |||  ||||  |||  |  |||||||
Db        104 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 163

Qy        140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
              |||||||  |||||  |  ||  |  ||||||||||||||  ||  |  ||  |||  ||||
Db        164 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 223

Qy        200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
              |  ||  ||||  ||||||  ||||||||||||||||||  ||  ||||||||||||||  ||||
Db        224 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 283

Qy        260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
              |  ||  ||  ||||||||  ||  ||  |||||  |  ||||||  ||  ||||  |||  |  ||||
Db        284 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 343

Qy        320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
              |  |||||||||  |||||  |  ||  ||  ||  ||||  |||||  ||  ||  ||  |||||||||
Db        344 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 403

Qy        380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGTATG 439
              |  |||||  |||||  |||  |  ||  ||  ||  ||  ||||  ||||||  ||||  ||  |||||||
Db        404 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 463

Qy        440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
              |  |||||  |||||  |  ||||  ||||||||||  ||||||||||  |  |||  |
Db        464 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 523

Qy        500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCA 559
               |||||||  |||  ||       ||  |||  |  ||  |||||    ||||||||  |||||||
Db        524 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 583

Qy        560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCTGGG 619
                 |||  |  ||  |   |||||||    ||    |||||  |  ||  ||||||||  |||||||
Db        584 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 643

Qy        620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
                  |  |||  |  ||||||||||  |||||||  ||  ||||||  |  ||  ||  |||  ||||  |
Db        644 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 703

Qy        680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
              |||||  |  |||||||    ||||  |||  |  ||  |||||  |||||  ||||||  |  ||  ||||
Db        704 CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA 763

Qy        740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG 799
              ||||  ||  ||  |  ||  |  |  |  |  |  ||  |||||||  ||          ||||  |
Db        764 TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC------TGCAGCCTGTTT 817

Qy        800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAG 859
                |  |  |  ||  |  |  |  ||  |||||  ||||  |  |||||||
Db        818 CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGAGCGCTGTGGCGGCTGAAA 877

Qy        860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
              |  ||||||||  ||  ||  |  |||||  |||  ||||  |||||||  |||||  ||||  |
Db        878 TAAAGCAGATCCGAGCCAGAAGGAAAACAAAACGGATGTTGATGGTTGTGCTTTTGGTAT 937
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Qy        920 TCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979
              | ||  | ||||| || || || ||| |||||||||| || ||||| || || |||||||
Db        938 TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 997

Qy        980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039
              |   |||  |    ||| | ||  |||| || ||||| || ||||| || |||||||| |
Db        998 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG 1057

Qy       1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGCAAATTCCGGG 1099
              | || ||||| || ||||| || || || || || || || || |||||||| ||||| || |
Db       1058 TATATGCCAATAGTGCTGCGAATCCAATTATTTATAATTTTCTCAGTGGAAAATTTCGAG 1117

Qy       1100 AGCAGTTTAAGGCTGCCTTCTC---CTGCTGCCTGCCTGGCCTGGGTCCCTGCGGCTCTC 1156
              || | ||||| ||||| || ||   ||| |||||    |  |    || |   |    ||
Db       1118 AGGAATTTAAAGCTGCGTTTTCTTGCTGTTGCCTTGGAGTTCACCATCGCCAGGAGGATC 1177

Qy       1157 TGAAGGCCCCTAGTCCCCGCTCCTCTGCCAGCCACAAGTCCTTGTCCTTGCAGAGCCGAT 1216
               |    ||    | |       | | |  ||||  ||||||||| ||   || | | |
Db       1178 GGCTCACCAGGGGACGAACTAGCACAGAGAGCCGGAAGTCCTTGACCACTCAAATCAGCA 1237

Qy       1217 GCT------CCGTCTCCAAAATCTCTGAGCATGTGGTGCTCACCAGCGTCACCACAGTGC 1270
               ||       | | || ||| | |||||||| || |||||||| ||| | | |||| | |
Db       1238 ACTTTGATAACATATCAAAACTTTCTGAGCAAGTTGTGCTCACTAGCATAAGCACACTCC 1297
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Search completed: October 16, 2004, 03:40:39
Job time : 663.145 secs